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OM nucleic - nucleic search, using sw model

Run on: May 29, 2002, 09:57:51 ; Search time 155.44 Seconds
(without alignments)
6770.074 Million cell updates/sec

Title: US-09-072-994A-13

Perfect score: 1019

Sequence: 1 ATGAAGTTGTCAGATTATTA.....TTACAAATTAATGTTGATTG 1019

Scoring table:

IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 822886 seqs, 516359360 residues

#Actl number of hits satisfying chosen parameters: 1645772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_MN_New:*
1: /cgn2_6/ptodata/1/pna/PC7_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
C	1	81.8	8.0	13859	6	US-10-105-299-12506
C	2	69.4	6.8	20420	6	US-10-103-295-385
C	3	66	6.5	13859	6	US-10-105-299-12506
C	4	63.2	6.2	20420	6	US-10-103-295-385
C	5	62.8	6.2	3252	6	US-10-027-632-113786
C	6	62.8	6.2	3252	6	US-10-027-632-113787
C	7	62.8	6.2	3252	6	US-10-027-632-113788
C	8	60.4	5.9	3252	6	US-10-027-632-113786
C	9	60.4	5.9	3252	6	US-10-027-632-113787
C	10	60.4	5.9	3252	6	US-10-027-632-113788
C	11	60.4	5.9	3252	6	US-10-027-632-113786
C	12	59.8	5.9	19965	6	US-10-103-295-384
C	13	56.8	5.6	5917	1	PCT-US02-06415-9
C	14	56.6	5.6	5563	6	US-10-136-734-26
C	15	56.2	5.5	628	6	US-10-027-632-113152
C	16	55	5.4	3991	6	US-10-074-045-60
C	17	53.8	5.3	418	5	US-09-789-189-613
C	18	53.4	5.2	755	6	US-10-027-632-128109
C	19	51.8	5.1	19965	6	US-10-103-295-384
C	20	51.6	5.1	3991	6	US-10-074-045-60
C	21	51	5.0	2053	6	US-10-027-632-97533
C	22	51	5.0	3996	1	PCT-US02-06415-42
C	23	50.8	4.9	2053	6	US-10-027-632-97533
C	24	50	4.9	405	5	US-09-789-189-1995
C	25	50	4.9	689	6	US-10-027-632-32696
C	26	50	4.9	689	6	US-10-027-632-32697

C	27	50	4.9	14809	1	PCT-US02-09186-914	Sequence 914, App
C	28	50	4.9	14809	1	PCT-US02-09370-950	Sequence 950, App
C	29	50	4.9	14809	6	US-10-105-299-6325	Sequence 6325, Ap
C	30	50	4.9	46843	6	US-10-105-299-13395	Sequence 13395, A
C	31	49.4	4.8	375	5	US-09-789-189-1457	Sequence 1457, Ap
C	32	49.4	4.8	755	6	US-10-027-632-128109	Sequence 128109,
C	33	49.2	4.8	1137	6	US-10-027-632-219520	Sequence 119520,
C	34	48.8	4.8	843	6	US-10-027-632-7034	Sequence 7034, Ap
C	35	48.4	4.7	529	5	US-09-789-189-835	Sequence 835, Ap
C	36	48.4	4.7	628	6	US-10-027-632-233402	Sequence 233402,
C	37	48.4	4.7	628	6	US-10-027-632-233403	Sequence 233403,
C	38	47.8	4.7	695	6	US-10-027-632-271551	Sequence 271551,
C	39	47.8	4.7	695	6	US-10-027-632-27031	Sequence 27031, A
C	40	47.8	4.7	858	6	US-10-027-632-154234	Sequence 154234,
C	41	47.6	4.7	534	6	US-10-027-632-242384	Sequence 242384,
C	42	47.6	4.7	534	6	US-10-027-632-242385	Sequence 242385,
C	43	47.6	4.7	534	6	US-10-027-632-242386	Sequence 242386,
C	44	47.6	4.7	628	6	US-10-027-632-113152	Sequence 113152,
C	45	47.6	4.7	3233	5	US-09-919-002-2106	Sequence 2106, Ap

ALIGNMENTS

RESULT	1
US-10-105-299-12506/C	
Sequence 12506, Application US/10105299	
GENERAL INFORMATION:	
APPLICANT: Rosen, et. al	
TITLE OF INVENTION: Human Secreted Proteins	
FILE REFERENCE: PS950	
CURRENT APPLICATION NUMBER: US/10/105, 299	
CURRENT FILING DATE: 2002-03-26	
NUMBER OF SEQ ID NOS: 15197	
Prior Application removed - See File Wrapper or Palm	
SOFTWARE: Patentln Ver. 2.0	
SEQ ID NO 12506	
LENGTH: 13859	
TYPE: DNA	
ORGANISM: Homo sapiens	
US-10-105-299-12506	
Query Match	8.0%; Score 81.8; DB 6; Length 13859;
Best Local Similarity	44.9%; Pred. No. 7.4e-05;
Matches 349; Conservative 0; Mismatches 427; Indels 1; Gaps 1;	
QY	107 AAATAGTTGATGAAGATTCAGTCTCCACCATTCATCCATCGAAGAAATTTTATAC
DB	7696 ATATAATATATCATATATATTAANTGTAATACCATATATATATATTTTATTC
QY	167 TTAACCTTGAACACCATCCAAACATTAATTTTAATGATCTTAATTTTATG
DB	7636 ATTAGATTTTAT
QY	227 ATGATGTTATATAGTCACCAATTTGATGCTATATGATTTGATGATTTGAATTA
DB	7576 GTTACATATTTAT
QY	287 CAATAATTTTAAACGACACGATTTATTAATGTTATATGTAATCTTTAGTA
DB	7516 TATTAATTTAT
QY	347 ATCAATATACACTTGCATATGAATTAAGAAAGATATCAATTTATGTTAAATCA
DB	7456 TAAATAAT
QY	407 TGAGTTGAGACTTGAATTTATTCATTCACAGGATATATCATGCTGATATAAACCA
DB	7396 AATTAATATATGCAATTTATATATATATATATATATATATATATATATATAT
QY	467 GTATATTTTCTTGGCCGATGATATATACACACGATTTATGAGATTTTGAATTT

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Db      7336 ATATTTTAAATAAATAATTATTAATATTAATATTAATTAATTAATTAATTAATCATATTAAT 7277
Qy      527 GTTAGATTTAAACCTGCCACCCTAAAGATGAACCCCTATGGCGAAATATAT -TGATGTA 585
Db      7276 AATATTTATTAATTAATAATAAAAAATTAATATGTTCATTACAATAATAATAAATATAT 7217
Qy      586 TCTACAGATTTTAAAGCACCAGAATTTGATCTCTGGATATCAATAATTATGAAATGA 645
Db      7216 ATTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 7157
Qy      646 ATTGATTTTTGGTCATTTGGGTATTAATTTTTGCATGCTTTATATATTCAGAAAATTTTCAAAGT 705
Db      7156 ATAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 7097
Qy      706 GTTTAGTCAAGATGATRAAGAAATTGACTATGTATCTCATGTTAGTAGATTAATTTTA 765
Db      7096 GATATATTAATTAATTAATTTATATATTAATTAATTAATTAATTAATTAATTAATTAATTA 7037
Qy      766 TTAAATCCAATTTTGAAGAAATTCGGTACACCACCAATTAACGTATTTGAGMATGAATTA 825
Db      7036 AAATATTAATTTATATATATATTAATTAATTAATTAATTAATTAATTAATTTTACATTTATTAAT 6977
Qy      826 TTTTGTGATGATATTAATTAATGAAGAACCTTGCACTTTTAAAAAATTCATTTTACAAAA 882
Db      6976 ACATTTATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 6920

RESULT          2
US-10-103-295-385
; Sequence 385, Application US/10103295
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: g1 Human Secreted Proteins
; FILE REFERENCE: PZO30PZ
; CURRENT APPLICATION NUMBER: US/100/103,295
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: PCT/US01/29871
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/00911
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/234,925
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 09/482,273
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: PCT/US99/15849
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,922
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,956
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 417
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 385
; LENGTH: 20420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-103-295-385
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Query Match	6.88;	Score 69.4;	DB 6;	Length 20420;
Best Local Similarity	44.18;	Pred. No. 0.0067;		
Matches 340;	Conservative 0;	Mismatches 426;	Indels 5;	Gaps 1;

OY	142	TCAATCCATCGAGAAATTTTATTACTTAAACCTTGAAAACCATCCAACTAATGTGAA	201
Db	4082	tacgcgcgccatatatgatataatatatatatagaaaaatatatatatatata	4141
OY	202	TATTTTAAGAATCTTAAATTTATGATGATGATATTTTGGTACCAGAAATGTATCCTTAT	261
Db	4142	tatatgaaaaaatatataaaatatatatbgaaaatatatatataaatatatgaa	4201

[illegible]

RESULT 3
US-10-105-299-12506
; Sequence 12506, Application US/10105299

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1  APPLICANT: Rosen, et. al
2  TITLE OF INVENTION: Human Secreted Proteins
3  FILE REFERENCE: P5950
4  CURRENT APPLICATION NUMBER: US/10/105,299
5  CURRENT FILING DATE: 2002-03-26
6  NUMBER OF SEQ. ID NOS: 15197
7  Prior Application removed - See File Wrapper or Palm
8  SOFTWARE: PatentIn Ver. 2.0
9  SEQ ID NO: 12506
10 LENGTH: 13859
11 TYPE: DNA
12 ORGANISM: Homo sapiens
13 US-10-105-299-12506

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Query Match	Score 66;	DB 6;	Length 13859;
6.58;			

[illegible]

Qy 73 ATTGATTAAGTTTAAATACCTTAACAGTATGCTTTAAATACTGATGAAGATTTCAAGTCTT 132
 || |||| | ||| ||| | ||| ||| | ||| |
 Db 6350 atagataataatatacttataataataataataataatataatgtaagaattgata 6405
 Qy 133 CCACACATTCATTCATCGAAGAAATTTTATCTTAAACCTTTGAAACCATCCCAAC 192

Qy	857	ATTTAAAAATTCATTTTCAAAAATATCCCTGAAAAGCTGGGATTTATTTTACGC	916
Db	4163	TTTATATATATTTTTCATATATATATATATATATTTTTCATATATATATATA	4104
Qy	917	GATGCAATGATG	928
Db	4103	TACATATATATG	4092

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RESULT      5
US-10-027-632-113786
Sequence 113786, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 113786
LENGTH: 3252
TYPE: DNA
ORGANISM: Human
US-10-027-632-113786

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Query Match	6.28;	Score 62.8;	DB 6;	Length 3252;
Best Local Similarity	44.68;	Pred. No. 0.072;		
Matches 379;	Conservative 0;	Mismatches 462;	Indels 9;	Gaps 3;

Oy	157	ATTTTTAACTTAATAACTTTGAACCAACCACATCAATGAAATTTTAAATCATCT	216
Dd	1154	aatttaataataacaactttaaaaaagcctaattatataatlaogtcaattaataacaactctt	12233
Oy	217	AAAAATTATGATGGATTTATATTA--GTCCACCAATTTGATCGTTAGTTTGAGTCAA	273
Dd	1224	tatacttaacgttaacttaataaaatlaaatlaataatagaatlaacttaataatagtc	12833
Oy	274	TTCATTGGAATTTACAAAATATTTGTAACGACACACAGTTTTATTATGATTTAATGCT	333
Dd	1284	taacctataataatagttaaacaatataaabaatalaatalaataataataatataat	13433
Oy	334	AATCGTTTAGTATCAATPTCACCTGCTAAAGAATTTGAAGAAAAGATTCACAATTA	393
Dd	1344	atataataatacatataataataaattgcatlacaattatataataacaataaaaacca	14033
Oy	394	TGGTTAAATCAATGAGCTTCAGACTTGGAATTATTCATTCACAAGGATTAATTCNGT	453
Dd	1404	attcataataatacaaatgataatttatataatcataatcataatagtlataataatacaaat	14633
Oy	454	GATATAAAAACCAAGTAATATTTTCTTTGCCCGGATGATATTAACAACAACCGATTATTGGA	513
Dd	1464	aataataaatactctataattataataagaagaatgaacaat-----attcaataataat	15183
Oy	514	GATTTTGATTTTGTGTTGATTTTAAACCTGCCACCTAAAGATGAACCCCCTATGGCGAA	573
Dd	1519	agatctccataataataatataatgaatatatgtaataaataatgatataatacaatca	15783

Qy	574	TATTTGATGATGATCTACAGAGTATTTTATTAAGCACACAGATTTGATTCCTGGATTAACGATT	633
Db	1579	ttatataataataaataattatataatlaataataataataataataataatctgtataatlaaat	1638
Qy	634	TATCAAAATGATAAATTGATATTGTTGGTCATTGGGTATTAAT-TTGGACTGGTTATATTCAGA	692
Db	1639	ataataataataaatttgtatataataataataataataataataataataataatctgtataatlaaat	1698
Qy	693	AAATTTTCCAAGTCTTTTACTCAAGATGATTAAGAAATTGACTAATGATTTCTCATGTTAG	752
Db	1699	ataataataataaanaatttgtataatlaaataataataataataataataataatctgtatlaaa	1758
Qy	753	TGATTTATTTATTTATTAATCAAAATTTGTAATAATTCGGTACACCAATTTTAACGATTT	812
Db	1759	ataataataataataaataatttgtatataataataataataataataataatctgtattataaataat	1818
Qy	813	TGAAGATGAATTTATTTGGTCATGATATATATAATGAAGAACTTGGCATTTTAAAAAATTCGA	872
Db	1819	ataataataataaatttgtattctgtaaataataataataataataataataatctgtattataaataat	1878
Qy	873	TTTTCAAAATATTCCTCGAAGAAAGATTGGGATATTATTTATTCCTCGATCGAATGATGATTT	932
Db	1879	aataataaataataataataataataataataataataataataataataataataataatgcaaatla	1938
Qy	933	AATGAAGAAATTTTTCACAAGATGATTGATATGATGATGCAAGTAAAGAAATTAACCTCTAA	992
Db	1939	tatatataataatacatgattatttatataattatataatttaataatttaataatctgtlaactaat	1998
Qy	993	AGAAATCTTA 1002	
Db	1999	ataataatgta 2008	

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RESULT      6
US-10-027-632-113787
; Sequence 113787, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;   Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113787
;   LENGTH: 3252
;   TYPE: DNA
; ORGANISM: Human
US-10-027-632-113787

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	Query Match	6.28;	Score 62.8;	DB 6;	Length 3252;
	Best Local Similarity	44.6%;	Pred. No. 0.072;		
	Matches 379;	Conservative	0;	Mismatches 462;	Indels 9; Gaps 3.
QY	157 AATTTTAACTTAATAAAGCTTGGAACCAATCCAAACATAATGAAATTGTAATGTCTT	216			

Db 1164 aatttaataatacatatataaaagcttaatttaatatattacgttaataataacaactct 1223
QY 217 AAAATTATGATGATGTTATATTA---GTCACCAAAATTGATCGTTATGATGTCAA 273
Db 1224 tatcttaccgttaacttaacttaaatlaataataglaaatlaacttaacttaaatatgc 1283
QY 274 TTGATTTCAAAATTTGTAACAAATTTGTAACGACAGATTTATTTATGATTTATGATG 333
Db 1284 taactatataatagtaacatataataatataataatataatagtaataatataatct 1343
QY 334 AATCTGTATGTAATCAATATACACTTGTCTAATGAAATTTGAGAAAAGATATCAATTA 393
Db 1344 atattataataatattataataatttgatcattacattattataataacaataaatca 1403
QY 394 TGGTAAATCAATGACTTGACAGCTTGATTTATTCATTCACAGAGGATTAATTCATCGT 453
Db 1404 attacaataatacaaatgataatctataaactataatagtaataataataacaatct 1463
QY 454 GATTTAAACCCAGTAAATATTTCTTTGCCGGGATGATTAACACACACGATTAATTTGA 513
Db 1464 aataataaattcttataataataataagaatagaacatct---attacataataat 1518
QY 514 GATTTGATATTTGTTGATTTTAAACCTGCCACCTAAGATGACCCCTATGGCGAA 573
Db 1519 agtatcatatcatatataatataatgataatgataatgataatgataatgataatgata 1578
QY 574 TATATGATGATGATGATGATGATTTTAAAGACACGAAATGATTTGATTAATCAAT 633
Db 1579 ttataataataataatataatataatataataataataatataatataatataatata 1638
QY 634 TATGAAATATGAAATTTGATTTGGTCAATTTGGGATTAAT-TTTCACCTGGTTATATTCAGA 692
Db 1639 atataataataataatataatataatataataataataataataatataatataat 1698
QY 693 AAATTTTCAAGTGTTTTACTCAAGATGATTAAGAAATTTGATTAATGATTTTCAATG 752
Db 1699 atataataataataatataatataatataataataataataataatataatataat 1758
QY 753 TGATTTATATTTTATTAATCAATATTTGAAATTTTCCGATCCCAATTTAATGATTT 812
Db 1759 atataataataataatataatataatataataataataataatataatataatata 1818
QY 813 TGAAGATGAAATTTTGTGATGATTAATTAATGAAATTTGATTTTAAATTTAAATTTGA 872
Db 1819 ataataataataatataatataatataataataataataatataatataatataat 1878
QY 873 TTTACAAAATATCTCTAGAAAAGATTTGGATATTTATTTTACCTCGATGCAATGATTT 932
Db 1879 aataataataataatataatataatataataataataataataataataatataat 1938
QY 933 AATGAAAGAAATTTTACCAAGATGATTAATGATGATCGAAGTAAAGAAATTAATCTCTAA 992
Db 1939 tatataataataatataatataatataatataatataatataatataatataat 1998
QY 993 AGAAATCTTA 1002
Db 1999 ataataagta 2008

RESULT 7
US-10-027-632-113788
; Sequence 113788, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 113788
; LENGTH: 3252
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-113788
Query Match 6.2%; Score 62.8; DB 6; Length 3252;
Best Local Similarity 44.6%; Pred. No. 0.072;
Matches 379; Conservative 0; Mismatches 462; Indels 9; Gaps 3;
QY 157 ATTTTATCTTAAACTTTGAAACCAATCCAAATTAATGATATTTTATGATCTT 216
Db 1164 aatttaataatacatatataaaagcttaatttaatatattacgttaataataacaactct 1223
QY 217 AAAATTATGATGATGTTATATTA---GTCACCAAAATTGATCGTTATGATGTCAA 273
Db 1224 tatcttaccgttaacttaacttaaatlaataataglaaatlaacttaacttaaatatgc 1283
QY 274 TTGATTTCAAAATTTGTAACAAATTTGTAACGACACGATTTATTTATGATTTATGATG 333
Db 1284 taactatataatagtaacatataataatataataataataatataatataatataat 1343
QY 334 AATCTGTATGTAATCAATATACACTTGTCTAATGAAATTTGAGAAAAGATATCAATTA 393
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QY 394 TGGTAAATCAATGACTTGACAGCTTGATTTATTCATTCACAGAGGATTAATTCATCGT 453
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QY 454 GATTTAAACCCAGTAAATATTTCTTTGCCGGGATGATTAACACACGATTAATTTGA 513
Db 1464 aataataaattcttataataataataagaatagaacatct---attacataataat 1518
QY 514 GATTTGATATTTGTTGATTTTAAACCTGCCACCTAAGATGACCCCTATGGCGAA 573
Db 1519 agtatcatatcatatataatataatgataatgataatgataatgataatgataatgata 1578
QY 574 TATATGATGATGATGATGATTTTAAAGACACGAAATGATTTGATTAATCAAT 633
Db 1579 ttataataataataatataatataatataataataataataatataatataatataat 1638
QY 634 TATGAAATATGAAATTTGATTTGGTCAATTTGGGATTAAT-TTTCACCTGGTTATATTCAGA 692
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QY 693 AAATTTTCAAGTGTTTTACTCAAGATGATTAAGAAATTTGATTAATGATTTTCAATG 752
Db 1699 atataataataataatataatataatataataataataataataatataatataat 1758
QY 753 TGATTTATATTTTATTAATCAATATTTGAAATTTTCCGATCCCAATTTAATGATTT 812
Db 1759 atataataataataatataatataatataataataataataataatataatataat 1818
QY 813 TGAAGATGAAATTTTGTGATGATTAATTAATGAAATTTGATTTTAAATTTGA 872
Db 1819 ataataataataatataatataatataataataataataatataatataatataat 1878
QY 873 TTTACAAAATATCTCTAGAAAAGATTTGGATATTTATTTTACCTCGATGCAATGATTT 932
Db 1879 aataataataataatataatataatataataataataataataatataatataat 1938
QY 933 AATGAAAGAAATTTTACCAAGATGATTAATGATGATCGAAGTAAAGAAATTAATCTCTAA 992
Db 1939 tatataataataatataatataatataatataatataatataatataatataat 1998
QY 993 AGAAATCTTA 1002
Db 1999 ataataagta 2008


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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-113788

Query Match      5.9%; Score 60.4; DB 6; Length 3252;
Best Local Similarity 46.6%; Pred. No. 0.17;
Matches 446; Conservative 0; Mismatches 491; Indels 21; Gaps 7;

QY 10 TCAGATATATATATAGACAGAAATTAATTTACAAATAGTGCACCTTCTGATATATACG 69
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Db 2567 TTAATATCTTATATATATCTTAATGTAATATATCTTATTTTAAAGTATACCTTAAAG 2508

QY 70 GCTATGTAAGTATTAATTAAGTACCGATGCTCTTAATAGTGAAGATTTAGT 129
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Db 2507 TATATTAATAGTATATTT--TTAATATCTATGCTTTAAAGTATTAAGTATACAT 2450

QY 130 CTTCACACCATTCATCATCGAGAAATTTTATCTTAAACCTTGAAACCATCA 189
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Db 2449 GAATATATTTAT-----ATATTAATACCTTAACACTTAAATATATATATATA 2396

QY 190 AACATATGTAATTTTAAATGATCTTAAATTTATGATGATATATTTAGTACCA 249
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2395 TACTTATACATAATTTTAAACCTTTAATATATGAAATTAATATATAGTTTAACT 2336

QY 250 TT-GTATGCTATGATTTGAGTCAATGATGAAATTCAAATATGTAACGACAA 308
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2335 TTAATATTTAAAGTATTAATTAATTAATCTAACAAATTTTATCTTATATATAGTT 2276

QY 309 AGCATTTATTTATGATTAATGTAATCTGTTAGTATCAATATACATGCTGTAATGA 368
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Db 2275 ATATGTTTATCTGTAATATATATTTAACTGATGTAACATGTAATAGTTATAT 2216

QY 369 AATTAAGAAAAAGTATCAATTTTGTGTTAAATCAATGATGACGACTTGATTTAT 428
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2215 ATTTAAATTTAATATATATATCTTAAATATTAATTTTAAACATATATCTAFA--TTCA 2158

QY 429 TCATTCACAAAGGATATTCATCGATATATAAACCCAGTAATTTTCTTGGCCGGGA 488
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2157 TAATTCATATTTATATATTTA-----ATATATAAATACCAATATATCTTATTA 2104

QY 489 TCATATACACACCGATATGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 548
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2103 TAATTTAATATATATATATATATATATATATATATATATATATATATATATAT 2047

QY 549 TAAAGATGAACCCCTATGCGAAATATATGATGATCTACAGTATTTATTAAGACC 608
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Db 2046 AATTTATATATATATATATATATATATATATATATATATATATATATATATAGT 1987

QY 609 AGAATGATTTGCTGATATCTAATTTATGAAATGAAATTTGCTGATTTGGGTAT 668
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1986 AATTTAAATATATATATATATATATATATATATATATATATATATATATATAT 1927

QY 669 AATTTGAGTGGTTTATCTCAGAAATTTTCAAGTGGTTAGTCAAGATGAAAGA 728
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Db 1926 TATTTATATATATATATATATATATATATATATATATATATATATATATATAT 1867

QY 729 ATTGACTAATGATTTCTCATGTTAGTATTAATTTATTTAAATCAATATTTGAAAAT 788
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Db 1866 AACAATATTTATATATATATATATATCAATTAACAATTTTATATATATATATATA 1807

QY 789 CGGTACACCAATTTAAGCATTTTGAAGTAAATTTTGGATGGAATATATTAAGA 848
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Db 1806 CAATTAATATATATATATATATATATATATATATATATATATATATATATAT 1747

QY 849 AACTTGCAATTTTAAATTTCAATTTCAAAATATCTGAGAAAGATTTGGATTTAT 908
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Db 1746 ATTTATATATATAT--ATATATTTTAAATATACAAATTTTATATATATATATATAT 1688

QY 909 TTTACCTGATGCAATGATGATTTAATGAAGAATTTTACCAGATGATTTAGATAT 966
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1687 AATATTTATATATATATATATATATATATATATATATATATATATATATATAT 1630
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RESULT 12
US-10-103-295-384
; Sequence 384, Application US/10103295
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P2
; CURRENT APPLICATION NUMBER: US/10/103.295
; PRIOR APPLICATION NUMBER: PCT/US01/29871
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/00911
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/234,925
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 09/482,273
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: PCT/US99/15849
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,922
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,956
; NUMBER OF SEQ ID NOS: 417
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 384
; LENGTH: 19965
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-103-295-384

Query Match      5.9%; Score 59.8; DB 6; Length 19965;
Best Local Similarity 44.0%; Pred. No. 0.22;
Matches 344; Conservative 0; Mismatches 432; Indels 5; Gaps 2;

QY 51 CATTTCTGATATATATACGCTTTGTTAGTTTATTAATCTTACCGTATGCTTAAAT 110
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4083 cactgcagccatataatgatatataatataatataatataatataatataatataat 4142

QY 111 AGTGATGAGATTTCTCGCTTCCACACATTCATCAATCGAAGAAATTTTATCTTAA 170
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4143 atatgaaaaatatataatataatataatataatataatataatataatataatgaa 4202

QY 171 AACTTTGAAACACATCCAAATTAATGATATTTTATGATCTTAAATTTATGATGA 230
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4203 atataataatataatataatataatataatataatataatataatataatataatg 4262

QY 231 TGTATATTTAGTCCCAATTTGTATCGTTATGATTTGAGTCATTTGTAATTTACAA 290
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Db 4263 aaatatataatataatataatataatataatataatataatataatataatataat 4322

QY 291 ATATTGTAACGAACACAGATTTATTTATGTTATTAATGTTATGTTATGTTATGTA 350
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Db 4323 atatg--aaatatataatataatataatataatataatataatataatataatg 4380

QY 351 ATATACCTTGTCTATGAAATTTGAAGAAAAGATATCAAAATTTATGTTTAAATCAAT 410
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Db 4381 aaatatataatataatataatataatataatataatataatataatataatataat 4440

QY 411 TTCAGACATTAATTTATCTTCCACAGGATTAATTCATCGATGATTAACCCAGTAA 470
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4441 atataataatataatataatataatataatataatataatataatataatataat 4500

QY 471 TATTTCTTTCGCCGGGATGATTAACCAACCGATTTTGGAGATTTGATATTTGTTA 530
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Db 4501 atataataatataatataatataatataatataatataatataatataatataat 4560

QY 531 TGATTTAACTGCCACCTTAAAGATGAACCCCTATGCGCAATATATTTGATGATCTAC 590
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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113152
; LENGTH: 628
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-113152
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Query Match

5.5%; Score 56.2; DB 6; Length 628;

Best Local Similarity 51.6%; Pred. No. 0.77; Matches 174; Conservative 1; Mismatches 159; Indels 3; Gaps 2;

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QY 683 TATATTCAAGAAATTTTCAAGAGTCTTTCAGTCAAGATGAATGAATGCTAATGATT 742
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Db 158 taataaagataataataataataataataataataataataataataataataataata 217
QY 743 CTCATGTTAGTATTATTTATTTATTAATCAAAATTTGAAATTTGCGTACACCAATT 802
    || || || || || || || || || || || || || || || || || || || ||
Db 218 attattaataataataataataataataataataataataataataataataataata 277
QY 803 TAACTGATTTTGAGATGA-ATTATTTTGTGATGAATATTAATGAAGAACTTGCAATTT 861
    || || || || || || || || || || || || || || || || || || || ||
Db 278 tatatttaataataataataataataataataataataataataataataataataata 337
QY 862 AAAAAATTCATTTTACAAAATATCCTAGAAAGATTGGATATTTTAACTCGATGC 921
    || || || || || || || || || || || || || || || || || || || ||
Db 338 taataataataataataataataataataataataataataataataataataataata 397
QY 922 AATGATGATTTTAATGAAGAAATTTTACCAAGATGATTAGATATGATGAATAAAGA 981
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Db 398 taataataataat--aatataattttaataataataataataataataataataataat 455
QY 982 ATAACTTCTAAGAAATCTTACAAATTAATGATGATTT 1018
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Db 456 ataataataataataataataataataataataataataataataataataataataat 492
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Search completed: May 29, 2002, 14:55:26
Job time: 17855 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 29, 2002, 09:55:11 ; Search time 3703.9 Seconds
(without alignments)
5952.094 Million cell updates/sec

Title: US-09-072-994A-13

Sequence: 1019
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

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SUMMARIES				
No.	Score	Query Length	ID	Description
1	1019	100.0	1019	US-09-072-994A-13
2	1019	100.0	1019	US-09-072-994A-13
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5	1004.6	98.6	1020	PCT-US02-03987-14283
6	1004.6	98.6	1020	US-09-463-965-1
7	1004.6	98.6	1020	US-10-032-585-6173
8	1004.6	98.6	1020	US-10-072-851-14283
9	1004.6	98.6	1020	US-09-259-128-4099
10	1004.6	98.6	1020	US-09-314-050-6173
11	1003	98.4	1038	US-09-248-796-4351
12	1003	98.4	1038	US-09-096-409-4351
13	262	25.7	262	US-09-127-461-6643
14	260.4	25.6	262	US-09-127-461-3655
15	258	25.3	260	US-09-127-461-6591
16	252.4	24.8	277	US-09-127-461-6291
17	221.8	20.5	51	US-09-127-461-4911
18	85.8	8.4	223320	US-09-242-679-528
19	85	8.3	1770	US-09-703-708-6286
20	85	8.3	1770	US-09-164-330-6286
21	85	8.3	1770	US-09-183-791-6286
22	83.6	8.2	1336	US-09-663-779-8205
23	82.8	8.1	899	US-09-565-306-24647
24	82.8	8.1	1016	US-09-207-458-33653
25	82.6	8.1	1143	US-09-207-458-36757
26	82	8.0	1770	US-09-703-708-6286
27	82	8.0	1770	US-09-164-330-6286
28	82	8.0	1770	US-09-183-791-6286
29	81.8	8.0	13859	US-09-950-083-10355
30	80.6	7.9	1326	US-09-663-779-8205
31	79	7.8	223320	US-09-242-679-528

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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32 77 7.6 192014 63 US-60-248-823-33 Sequence 33, Appl
33 76.2 7.5 98573 63 US-60-248-505-542 Sequence 542, App
34 75.6 7.4 1033 28 US-09-705-826-16063 Sequence 16063, A
35 75.4 7.4 1680 16 US-09-248-796-4378 Sequence 4378, Ap
36 75.4 7.4 1680 48 US-60-096-409-4378 Sequence 19056, A
37 75 7.4 11062 56 US-60-173-464-19056 Sequence 1, Appl
38 74.6 7.3 1744 17 US-09-387-720-1 Sequence 33, Appl
39 74.6 7.3 1744 48 US-60-248-823-33 Sequence 433, App
40 74.6 7.3 192014 63 US-60-234-446-433 Sequence 22, Appl
41 74.4 7.3 32768 62 US-09-806-708-172 Sequence 17, Appl
42 74.2 7.3 1141 31 US-60-245-228-172 Sequence 36950, A
43 73.8 7.2 22350 63 US-60-207-458-36950 Sequence 774, App
44 73.4 7.2 1190 59 US-09-666-355A-774
45 73.2 7.2 988 26

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ALIGNMENTS

RESULT 1
US-09-072-994-13

; Sequence 13, Application US/09072994

; GENERAL INFORMATION:

; APPLICANT: Cottarel, Guillaume

; APPLICANT: Damagnez, Veronique

; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins from

; TITLE OF INVENTION: Human Pathogens, and Uses Related Thereto

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley, Hoag & Eliot, LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII (text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/072,994

; FILING DATE: 05-MAY-1998

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: MIV032.02

; INFORMATION FOR SEQ. ID NO.: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1019 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: linear

; MOLECULE TYPE: CDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1017

; US-09-072-994-13

Query Match 100.0%; Score 1019; DB 14; Length 1019;
Best Local Similarity 100.0%; Pred. No. 9.8e-159; Indels 0; Gaps 0;
Matches 1019; Conservative 0; Mismatches 0;

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QY 1 ATAAAGTTGTCAGATTATATATAGACAGATTATATTAACAATAGTCCATTCTGAT 60
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Db 1 ATGAAGTTGTCAGATTATATATAGACAGATTATATTAACAATAGTCCATTCTGAT 60
QY 61 ATATATACGGCTATTTGATAGTTTAATTAACCTACAGATGCTTAAATTAAGTTGATGA 120
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Db 61 ATATATACGGCTATTTGATAGTTTAATTAACCTACAGATGCTTAAATTAAGTTGATGA 120

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QY 121 GATTCAGTCTTCCACACATTCATCATCGAGAAATTTTATCTTAAACTTTGAAA 180
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Db 121 GATTTCAGTCTTCCACACATTCATCATCGAGAAATTTTATCTTAAACTTTGAAA 180
QY 181 CCACATCCAAACATTAATTTGAATTTTAAATGATCTTAAATTTGANGAGTGTATATTA 240
   |||||||
Db 181 CCACATCCAAACATTAATTTGAATTTTAAATGATCTTAAATTTGANGAGTGTATATTA 240
QY 241 GTACCAAAATTTGATGTTATGATTTGATGCAATTTGATTAATTAACAAATATTTGAAA 300
   |||||||
Db 241 GTACCAAAATTTGATGTTATGATTTGATGCAATTTGATTAATTAACAAATATTTGAAA 300
QY 301 CGAACAAACAGATTTTATTTATGTTAAATGTTAAATCTTGTAGTAATCAATACACTT 360
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QY 361 GCTAATGAATTTGAAGAAAAGATATCAATTTTGGTTAAATTCATGATGAGTCACTT 420
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Db 361 GCTAATGAATTTGAAGAAAAGATATCAATTTTGGTTAAATTCATGATGAGTCACTT 420
QY 421 GAATTTATTCATTCACAGAGGATTAATTCATCGATATTAACCCAGTAATATTTCTTT 480
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Db 421 GAATTTATTCATTCACAGAGGATTAATTCATCGATATTAACCCAGTAATATTTCTTT 480
QY 481 GCCCGGATGATATTAACACACAGGATTTTGGAGTTTGATATTTGTTATGATTTAAA 540
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Db 481 GCCCGGATGATATTAACACACAGGATTTTGGAGTTTGATATTTGTTATGATTTAAA 540
QY 541 CTGCGACCTTAAGATGACCCCTATGCGGAATTAATTTGATGATCTACAGTATTTAT 600
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Db 541 CTGCGACCTTAAGATGACCCCTATGCGGAATTAATTTGATGATCTACAGTATTTAT 600
QY 601 AAAGCACCAGAAATGATTTCTGTTATTAATTAATTAATTAATTAATTAATTTGTTGA 660
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Db 601 AAAGCACCAGAAATGATTTCTGTTATTAATTAATTAATTAATTAATTAATTTGTTGA 660
QY 661 TTGGGTATTAATTTGATGCTGTTATTAATTAATTAATTAATTTGTTGAATTAATTA 720
   |||||||
Db 661 TTGGGTATTAATTTGATGCTGTTATTAATTAATTAATTAATTTGTTGAATTAATTA 720
QY 721 GATTAAGAAATTTGATTAATTTGATTAATTTGATTAATTTGATTAATTTGATTAATTT 780
   |||||||
Db 721 GATTAAGAAATTTGATTAATTTGATTAATTTGATTAATTTGATTAATTTGATTAATTT 780
QY 781 GAAATTTGCTGTCACCCATTTAATGATTTTGAAGATTAATTTTCTGATGAATAT 840
   |||||||
Db 781 GAAATTTGCTGTCACCCATTTAATGATTTTGAAGATTAATTTTCTGATGAATAT 840
QY 841 AATATGAAAACCTGCAATTTTAAATTAATTTCAATTTCAAAAATATCTGAAAAAGATTGG 900
   |||||||
Db 841 AATATGAAAACCTGCAATTTTAAATTAATTTCAATTTCAAAAATATCTGAAAAAGATTGG 900
QY 901 GATATTAATTTTACCTGATGATGATTAATTAATTAATTAATTTTACCAAGATGATT 960
   |||||||
Db 901 GATATTAATTTTACCTGATGATGATTAATTAATTAATTAATTTTACCAAGATGATT 960
QY 961 AGATATGATGCAATTAAGAAATTAATTAATTTTAAAGAAATCTTAATTAATTTGATGATT 1019
   |||||||
Db 961 AGATATGATGCAATTAAGAAATTAATTAATTTTAAAGAAATCTTAATTAATTTGATGATT 1019

```

RESULT 2

US-09-072-994a-13

; Sequence 13, Application US/09072994A

; GENERAL INFORMATION:

; APPLICANT: Cottarel, Guillaume

; APPLICANT: Damagnez, Veronique

; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins from

; TITLE OF INVENTION: Human Pathogens, and Uses Related Thereto

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley, Hoag & Eliot, LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,994A
FILING DATE: 05-May-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/463,090
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-032.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-7000
TELEFAX: 617-832-1000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1017
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-072-994a-13

Query Match 100.0%; Score 1019; DB 14; Length 1019;
Best Local Similarity 100.0%; Pred. No. 9,8e-159;
Matches 1019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAGTTGCAGATTTATATAGACAGAGATTAATTACAAATGTCCTTCTGAT 60
E3 1 ATGAAGTTGCAGATTTATATAGACAGAGATTAATTACAAATGTCCTTCTGAT 60
QY 61 ATATATACGGCTATGTATAGATTAACTACAGATATGCTTAAATAGTGTGATA 120
Db 61 ATATATACGGCTATGTATAGATTAACTACAGATATGCTTAAATAGTGTGATA 120
QY 121 GATTTCAGTCTCCACACATTCATCCAGGAATTTTATACCTTAAACCTTTGAAA 180
Db 121 GATTTCAGTCTCCACACATTCATCCAGGAATTTTATACCTTAAACCTTTGAAA 180
QY 181 CCACATCCAAACATTAATGAAATTTTAAATGATCTTAAATTTATGATGATTTATATTA 240
Db 181 CCACATCCAAACATTAATGAAATTTTAAATGATCTTAAATTTATGATGATTTATATTA 240
QY 241 GTCAACCAATTTGATCTTATGATTTGAGTCAATTCATTGAAATTAACAAATATGTATAA 300
Db 241 GTCAACCAATTTGATCTTATGATTTGAGTCAATTCATTGAAATTTCAAAATATGTATAA 300
QY 301 CGAACACACAGATTTATTTGATTAATGTAATCTTGTTAGTATCAATATACACTT 360
Db 301 CGAACACACAGATTTATTTGATTAATGTAATCTTGTTAGTATCAATATACACTT 360
QY 361 GCTATATCAAAATGAGAAAAAGATATCAAAATTAATGCTTAAATCAATATGAGACTT 420
Db 361 GCTATATCAAAATGAGAAAAAGATATCAAAATTAATGCTTAAATCAATATGAGACTT 420
QY 421 GAATTTTTCATTCACAGGATTAATTCATCGATATTAACCCGATTAATTTTCTTT 480
Db 421 GAATTTTTCATTCACAGGATTAATTCATCGATATTAACCCGATTAATTTTCTTT 480

Db 421 GAATTTTTCATTCACAGGATTAATTCATCGATATTAACCCGATTAATTTTCTTT 480
QY 481 GCCCGGATGATTAATACACACAGATTTATGAGATTTGATATTTGATGATTTAAA 540
Db 481 GCCCGGATGATTAATACACACAGATTTATGAGATTTGATATTTGATGATTTAAA 540
QY 541 CTGCCACCTTAAGATGACACCCCTATGCGGAATTAATGATATCTACAGATTTAT 600
Db 541 CTGCCACCTTAAGATGACACCCCTATGCGGAATTAATGATATCTACAGATTTAT 600
QY 601 AAGACACAGATTTGATTTCTGTTATTAATTAATGATATGATGATATTTGATCA 660
Db 601 AAGACACAGATTTGATTTCTGTTATTAATTAATGATATGATGATATTTGATCA 660
QY 661 TTGGGTATTAATTTGACGTGTTATATTCAGAAATTTTCAAGTGTTTTACTCAAGAT 720
Db 661 TTGGGTATTAATTTGACGTGTTATATTCAGAAATTTTCAAGTGTTTTACTCAAGAT 720
QY 721 GATTAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db 721 GATTAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 781 GAAATTTGCGTACACCCATTTAATCTGATTTGAAGATGAATTAATTTGATGATAT 840
Db 781 GAAATTTGCGTACACCCATTTAATCTGATTTGAAGATGAATTAATTTGATGATAT 840
QY 841 AATATGAAGATTTGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
Db 841 AATATGAAGATTTGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
QY 901 GATATATTTTACCTGATGCAATGATGATGATGATGATGATGATGATGATGAT 960
Db 901 GATATATTTTACCTGATGCAATGATGATGATGATGATGATGATGATGATGAT 960
QY 961 AGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1019
Db 961 AGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1019

RESULT 3
US-09-305-929-13
Sequence 13, Application US/09305929
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Cyclin Activating Kinase (CAK) from Human
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/305,929
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/463,090
FILING DATE: 05-JUN-1995
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1017
US-09-305-929-13
Query Match 100.0%; Score 1019; DB 17; Length 1019;
Best Local Similarity 100.0%; Pred. No. 9,8e-159;
Matches 1019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGTTGTCAGATTATATATAGACAGAAATTATTTACAATAGTGCATTTCTGAT 60
 Db 1 ATGAGTTGTCAGATTATATATATAGACAGAAATTATTTACAATAGTGCATTTCTGAT 60
 QY 61 ATATATACGGGTATGTAAGTTAATACTTACCAATAGTCTTAATAAGTTGATGA 120
 Db 61 ATATATACGGGTATGTAAGTTAATACTTACCAATAGTCTTAATAAGTTGATGA 120
 QY 121 GATTTCAGTCTTCGACACATTCATCCATGAGAAATTTTATCTTAATAACTTTGAA 180
 Db 121 GATTTCAGTCTTCGACACATTCATCCATGAGAAATTTTATCTTAATAACTTTGAA 180
 QY 181 CCACATCCAAACATTAATGATATTTTAATGATCTTAATAATTTTGATGATGATTA 240
 Db 181 CCACATCCAAACATTAATGATATTTTAATGATCTTAATAATTTTGATGATGATTA 240
 QY 241 GTCACCAAAATTTGATCGTTATGATTTGAGTCATGATTTGAATTTACAAATATTTGAAA 300
 Db 241 GTCACCAAAATTTGATCGTTATGATTTGAGTCATGATTTGAATTTACAAATATTTGAAA 300
 QY 301 CGAACACACATTTATTTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 360
 Db 301 CGAACACACATTTATTTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 360
 QY 361 GCTAATGAATTTGAAGAAAGAAATATCAAAATTTATGTTAAATCAATGATTCAGACTT 420
 Db 361 GCTAATGAATTTGAAGAAAGAAATATCAAAATTTATGTTAAATCAATGATTCAGACTT 420
 QY 421 GAATTTATTCATTCACAGGATTAATTCATGATTAATTAATTAATTAATTAATTAATTAATTA 480
 Db 421 GAATTTATTCATTCACAGGATTAATTCATGATTAATTAATTAATTAATTAATTAATTAATTA 480
 QY 481 GCGCGGATGATTAATTAACACACCGATTAATGATTAATGATTAATGATTAATGATTAATTA 540
 Db 481 GCGCGGATGATTAATTAACACACCGATTAATGATTAATGATTAATGATTAATGATTAATTA 540
 QY 541 CTGCCACCTAAGATGAACCCCTATGSCGAATATATTTGATTTGATTCACAGATTTTAT 600
 Db 541 CTGCCACCTAAGATGAACCCCTATGSCGAATATATTTGATTTGATTCACAGATTTTAT 600
 QY 601 AAAGCACCAGATTTGATTTCTGTTATGATTAATGATTAATGATTAATGATTAATGATTA 660
 Db 601 AAAGCACCAGATTTGATTTCTGTTATGATTAATGATTAATGATTAATGATTAATGATTA 660
 QY 661 TTGGGTATTAATTTTGAATGATTTTATTAATTCAGAAAATTTTCAAAAGTGTGTTAGTCAAGAT 720
 Db 661 TTGGGTATTAATTTTGAATGATTTTATTAATTCAGAAAATTTTCAAAAGTGTGTTAGTCAAGAT 720
 QY 721 GATTAAGATTTGATTAATGATTTCTGATTTGATTAATTTTAAATCAATATTTT 780
 Db 721 GATTAAGATTTGATTAATGATTTCTGATTTGATTAATTTTAAATCAATATTTT 780
 QY 781 GAAAATTTGATTAATGATTTCTGATTTGATTAATTTTAAATCAATATTTT 840
 Db 781 GAAAATTTGATTAATGATTTCTGATTTGATTAATTTTAAATCAATATTTT 840
 QY 841 AATTAATGAACCTTGATTTTAAATAATTTCAATTTTCAAAATTTTCAAAATTTTCAAAATTTT 900
 Db 841 AATTAATGAACCTTGATTTTAAATAATTTCAATTTTCAAAATTTTCAAAATTTTCAAAATTTT 900
 QY 901 GATTAATTTTATTCATGATTAATGATTTTAAATGATTTTAAATGATTTTAAATGATTTT 960
 Db 901 GATTAATTTTATTCATGATTAATGATTTTAAATGATTTTAAATGATTTTAAATGATTTT 960
 QY 961 AGATATGATGAAGTAAAGAAATTAATCTTAAGAAATTTTCAATTAATTTGATTTGATTTG 1019
 Db 961 AGATATGATGAAGTAAAGAAATTAATCTTAAGAAATTTTCAATTAATTTGATTTGATTTG 1019

RESULT 4
 US-09-305-929A-13
 ; Sequence 13, Application US/09305929A

GENERAL INFORMATION:
 APPLICANT: BERLIN, VIVIAN
 APPLICANT: COMPEL, GUILLAUME
 TITLE OF INVENTION: CYCLIN ACTIVATION KINASE (CAK) FROM HUMAN PATHOGENS,
 TITLE OF INVENTION: AND USES RELATED THEREO
 FILE REFERENCE: MIV-032.03
 CURRENT APPLICATION NUMBER: US/09/305.929A
 PRIOR FILING DATE: 1999-05-05
 PRIOR APPLICATION NUMBER: 09/072.994
 PRIOR FILING DATE: 1998-05-05
 PRIOR APPLICATION NUMBER: 08/463.090
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO 13
 LENGTH: 1019
 TYPE: DNA
 ORGANISM: Candida sp.
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1017)
 US-09-305-929A-13

Query Match 100.0% Score 1019; DB 17; Length 1019;
 Best Local Similarity 100.0%; Pred. No. 9.8e-159;
 Matches 1019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGTTGTCAGATTATATATAGACAGAAATTATTTACAATAGTGCATTTCTGAT 60
 Db 1 atgaagtlgctgagatattatattatagacagaaatttttacaatagtgccatttctgat 60
 QY 61 ATATATACGGGTATGTAAGTTAATACTTACCAATAGTCTTAATAAGTTGATGA 120
 Db 61 atatacgcgtatgtaagtttaataactttaccagttatgctttaaaatagtgatgaa 120
 QY 121 GATTTCAGTCTTCGACACATTCATCCATGAGAAATTTTATCTTAATAACTTTGAA 180
 Db 121 gatttcagtcttcacacatttcacatccatgagaaatttttatactttaaaactttgaaa 180
 QY 181 CCACATCCAAACATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 240
 Db 181 ccacatccaaacataatltgatatlttaatgaltcttaaaatltatgaltgatatata 240
 QY 241 GTCACCAAAATTTGATCGTTATGATTTGAGTCATGATTTGAATTTTCAAAATTTTGA 300
 Db 241 gtccacaaatgtatgctgattgattgagtcattgattgaatttcataaactttgtaa 300
 QY 301 CGAACACACATTTATTTATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 360
 Db 301 cgaaacacagatttattatgtattgattgattgattgattgattgattgattgattgatt 360
 QY 361 GCTAATGAATTTGAAGAAAGAAATATCAAAATTTATGTTAAATCAATGATTCAGACTT 420
 Db 361 gctaataaattgaagaaagaaatatacaaatltatgltlaaaacaatgtgtcaagact 420
 QY 421 GAATTTATTCATTCACAGGATTAATTCATGATTTTAAATGATTTTAAATGATTTTAA 480
 Db 421 gaatttattcattcacaggaattatcattcattcattcattcattcattcattcattcatt 480
 QY 481 GCGCGGATGATTAATTAACACACCGATTAATGATTAATGATTAATGATTAATGATTA 540
 Db 481 gcccgagatgatatatacaacacagattatcgagatttgaatttgaatttgaatttga 540
 QY 541 CTGCCACCTAAGATGAACCCCTATGSCGAATATATTTGATTTGATTCACAGATTTTAT 600
 Db 541 ctgccacctaaagatgaacccctatgscgaattatgataatgataatgataatgataat 600
 QY 601 AAAGCACCAGATTTGATTTCTGTTATGATTAATGATTAATGATTAATGATTAATGATTA 660
 Db 601 aaagcaccagatgtattcttgatataactaattatgaaatgaaatgtattcttgatata 660
 QY 661 TTGGGTATTAATTTTGAATGATTTTATTAATTCAGAAAATTTTCAAAAGTGTGTTAGTCAAGAT 720

Db 661 ttgggtataatttgcagtggtatattacagaataattccaagtgcttagtcaagaat 720
Qy 721 GATAAAGAAATTCAGTAATGATTCATGTAGTATATATATTAATTAACAATATTT 780
Db 721 gataaagaattgcaactaagatctcactgtagtgatattatattcaacaatattt 780
Qy 781 GAAAAATTCGTACACCCCAATTTAACTGATTTTGAAGATGATTTTGTGATGAATAT 840
Db 781 gaaaatttcgtagcaccacatttaactgatttgaagatgattatttcttgatgaat 840
Qy 841 AATAATGAACCTGCAATTTTAAAAAATTCATTTACAAAAATCTCTAGAAAAATTTGG 900
Db 841 aataatgaanaactgcatcttaaaaaattcaattcaaaaaatacctagaanaagattg 900
Qy 901 GATATATATTTTACCTCGATGCAATGATGATTTAAATGAAGAAATTTTACCAAGATGAT 960
Db 901 gatattatttaccctcgatcgatgattgatttaagaagaatttctcaagaatgatt 960
Qy 961 AGATATGATCGAAGTAAAGAAATTAATCTTAAGAAATCTTCAATTAATGTTGGATTG 1019
Db 961 agatatgacgaagtaaaaaagaataacttctaagaanaattcttaactaattgtagtg 1019

RESULT 5
PCT-US02-03987-14283
; Sequence 14283, Application PC/TUS0203987
; GENERAL INFORMATION:
; APPLICANT: Elittra Pharmaceuticals, Inc.
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
; FILE REFERENCE: ELITTRA 038VPC
; CURRENT APPLICATION NUMBER: PCT/US02/03987
; CURRENT FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14283
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Candida albicans
PCT-US02-03987-14283

Query Match 98.6%; Score 1004.6; DB 1; Length 1020;
Best Local Similarity 99.1%; Pred. No. 2.3e-156;
Matches 1010; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ATGAAGTTGTCAGATTTATATATGACAGGAATTAATTACAAATAGTGCATTTCGAT 60
Db 1 atgaagttgccaagatctatataagacaaggaatttaactaagtgccatttcgat 60
Qy 61 ATATATACGGGTATTTGATTAAGTTTAATTAAGTACAGTATGCTTAAATAGTTGATGA 120
Db 61 atataacggtatgttaagtttaacttaacttaaccagtagctcttaaaatagttgatga 120
Qy 121 GATTTCAGTCTTCACACACATTCATCCATCGAGAGAAATTTTACTTAAACTTTGAAA 180
Db 121 gatttcagctctccacacacatcaatccatcgaagttcttactaactaaacttgaaa 180
Qy 181 CCACATCCAAACATTAATTTGAATATTTTAATGATCTTAAATTTATGATGTTATATTA 240
Db 181 ccaatccaaaacataatattgataatttaacgaccttaaaatttgtagcgatataatta 240
Qy 241 GTCAACCAATTTGATGTTTATGATTTGAGTCAATTTGAAATTTCAAAAATTTGTAA 300
Db 241 gtccaacaaattgtagttagtttagtgcaatttgtagtgaattcaaaaatttgtaa 300
Qy 301 CGAACAACAGATTTATTTATGATTAATGTAATCTTGTGTGTAATCAATTAACACTT 360
Db 301 cgaacaacagatttattatgtagttagtgaattcttgtagtgaattcaataatacatt 360

Qy 361 GCTAATGAATTTGAGAAAAAGATATCAATTAATGTTAAATCAATGATTCAGACTT 420
Db 361 gctaataaattgaagaaaaagataccaactatcggttaaaatcaatgagttcaagact 420
Qy 421 GAATTTATTCATTACAAAGGATTAATTCATCTGATATTAACCAAGTATATTTCTTT 480
Db 421 gaatttatctatccaaggataattatcatcgtagtataaaccatataatttctt 480
Qy 481 GCCCGGATATATTAACACACCGGATTTATTTGAGATTTTGTATTTGTTATGATTTAAA 540
Db 481 gcccggaatgataacaacacgattatgagatttgatattgattagttatgattaaaa 540
Qy 541 CTCGACACTTAAGATGAACCCCTATGCGCAATTAATGATGATCTACAGGTATTTAT 600
Db 541 ctgcacacttaagaatgaaacccctatggcgaataatattgacgtaacaggtattat 600
Qy 601 AAAGCACAGATTTGATTTCTGTTATTAATTAATGAATTAATGAATTTGTTGTTCA 660
Db 601 aaagcacagaaattgattcttctgtataactaattatgaatagaattgatatctgtca 660
Qy 661 TTGGGTATATTTTGAAGTGTATTAATTCAGAAAAATTTTCAAGTGTATTGACAAAGT 720
Db 661 ttgggtataatttgaagtggttataatcagaaaaatttccaagtgcttagtcaagaat 720
Qy 721 GATTAAGAAATTTGACTATGATTTCTCATGTTAGTATTAATTTAATCAAAATATT 780
Db 721 gataaagaatttgactaattgattctcactgtagtgattatattatataataattt 780
Qy 781 GAAAAATTTGGTACACCAATTTAACTGATTTTGAAGATGAATTTTGTGATGAATAT 840
Db 781 gaaaatttcgtagcaccacatttaactgatttgaagaagaatttcttgatgaat 840
Qy 841 AATAATGAACACTTGATTTTAAAAAATTCATTTCAAAAATPACCTGAAAAATTTGG 900
Db 841 aataatgaanaacttgatctttaaataatccaatttaacaaatccctagaanaagattg 900
Qy 901 GATTAATTTTACCTCGATGCAATGATTTAATGMAAGAAATTTTACCAAGATGAT 960
Db 901 gatattatttaccctcgatcgatgatttctcatgaaagaatttcttaaccaagtgatt 960
Qy 961 AGATATGATCGAAGTAAAGAAATTAATCTTAAGAAATCTTCAATTAATGTTGATTTG 1019
Db 961 agatatgacgaagtaaaaaagaataacttctaagaanaattcttaactaattgtagtg 1019

RESULT 6
US-09-463-962-1
; Sequence 1, Application US/09463962
; GENERAL INFORMATION:
; APPLICANT: FAYE, GERARD
; APPLICANT: VALAY, JEAN-GABRIEL
; APPLICANT: MANN, CARL
; APPLICANT: THURET, JEAN-YVES
; TITLE OF INVENTION: KINASE ACTIVATING DEPENDENT CYCLIN PROTEIN KINASES AND THEIR
; FILE REFERENCE: 0846-0536-0XPCT
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: PCT/FR98/01788
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: FR97/10287
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1020)
US-09-463-962-1

Query Match 98.6%; Score 1004.6; DB 18; Length 1020;
Best Local Similarity 99.1%; Pred. No. 2.3e-156;
Matches 1010; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```
QY 1 ATGAAGTTGTCAGATTATATATATAGACAAAGAAATTAATTTCAATATAGTCCATTCTGAT 60
  |||||
Db 1 atgaagttgcagattatattatataagacaagaatattcaaatagcgcatcttcgat 60
QY 61 ATATATACGGCTATTTGATTAATGTTTAAATCTTACCATGATGCTTAAATAGTTGATGAA 120
  |||||
Db 61 atataatgacgtatgataaagtttaataactaccagatgcttcaaaaatagttgataa 120
QY 121 GATTTCAGCTTCCACCATTCATTCATCGACGAAATTTTATACCTTAAACCTTGAA 180
  |||||
Db 121 gatttcagcttccacccatccatccatcgagaagttcttatcttaaaacttga 180
QY 181 CCACATCCAAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 240
  |||||
Db 181 ccacatccaaacataatgaatatttaagatgacttaaaatttgacgataatatta 240
QY 241 GTACCAAAATTTGATCGTATGATTTGATGATTTGATGATTTGATGATTTGATGATTTGAT 300
  |||||
Db 241 gtacccaatctgacgtatgataatgacgtatgataatgataatgataatgataatgataa 300
QY 301 CGAACAACACGATTTATTTATGTTATGTTATGTTATGTTATGTTATGTTATGTTATGTTAT 360
  |||||
Db 301 cgaacaacacgatttattatgattatgattatgattatgattatgattatgattatgattat 360
QY 361 GCTAATGAATTTGAAGAAAACATATCAATTAATGTTAAATCAATGATGATGATGATGAT 420
  |||||
Db 361 gctaatgaatctgagaagaaagatacaatattggttaaaatcaatgattcagactt 420
QY 421 GATTTATTCATTTCCACCAAGGATTAATTCATGATTTAAACCCAGATTTATTTCTTT 480
  |||||
Db 421 gatattatcatcacaagggataatcatcgtgataataaaccagtaattcttctt 480
QY 481 GCCCGGATGATTAACACACCGATTAATTTGAGATTTTGAATTTTGAATTTTGAATTTTGA 540
  |||||
Db 481 gcccggaatgataataacacacgattattggaatttggatattgattatgattataa 540
QY 541 CTGCCACCTAAAGATTAACCCCTATGCGGAATTAATTAATTAATTAATTAATTAATTAAT 600
  |||||
Db 541 ctgccacctaagaatgaaacccctatgcggaataatataatgataatgataatgataat 600
QY 601 AAAGCACCAGATTTGATTTGTTGTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 660
  |||||
Db 601 aaagcaccagatctgattcttggtataactaatatgaatgaatgaatgaatgaatgaat 660
QY 661 TTGGGTATTAATTTGACTGGTTTATATTCAGAAAATTTTCAAAAGTTTACTCAAAAGAT 720
  |||||
Db 661 ttgggtataatttgactggttataatcaagaatatttcaaaagttttagtcaagat 720
QY 721 GATAAAGATTTGCTATGATTTCTCATGTTAGTGAATTTATTTTATTAATTAATTAATTT 780
  |||||
Db 721 gataaagaattgactaagatcttcctcgttgaatgattatattatataatcaatattt 780
QY 781 GAAATTTTGGTACACCCCAATTTTAACTGATTTTGAAGATTAATTTTGTGTAATTAAT 840
  |||||
Db 781 gaaatttcgtacaccccaatttaactgatttgaagatgaattatttcttgatgaat 840
QY 841 AATTAAGAAAATCTTGCAATTTTAAAAAATTCATTTTCAAAAATATCTTGAAAAAGATTGG 900
  |||||
Db 841 aataaagaatcttgcatctttaaataatcaatttcaaaaaatctcctaagaagattg 900
QY 901 GATATATTTTACCTCGATGACCAATGATGATTTAATGAAGAATTTTTCACCAAGATGAT 960
  |||||
Db 901 gatataatttaccctcgacgaatgataatgattcaatgaagaatcttctccagaatgatt 960
QY 961 AGATATGATCGAAGTAAAGAAATTAATCTTAAAGAAATCTTCAAAATTAATTTGTTGAT 1019
  |||||
Db 961 agtatatgacgaagtaagaatgaatcttcaagaagaatcttcaaatgaattgtagtg 1019
```

RESULT 7

US-10-032-585-6173

Sequence 6173, Application US/10032585

GENERAL INFORMATION:

APPLICANT: Terry, Roemer D.

APPLICANT: Bo, Jiang

APPLICANT: Charles, Boone

APPLICANT: Howard, Bussey

TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

FILE REFERENCE: 10182-005-999

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 8000

SOFTWARE: Patent version 3.1

SEQ ID NO 6173

LENGTH: 1020

TYPE: DNA

ORGANISM: Candida albicans

US-10-032-585-6173

Query Match 98.6%; Score 1004.6; DB 37; Length 1020;
Best Local Similarity 99.1%; Pred. No. 2.3e-156;
Matches 1010; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```
QY 1 ATGAAGTTGTCAGATTATATATATAGACAAAGAAATTAATTTACAATATAGTCCATTCTGAT 60
  |||||
Db 1 atgaagttgcagattatattatataagacaagaatattcaaatagcgcatcttcgat 60
QY 61 ATATATACGGCTATTTGATTAATGTTTAAATCTTACCATGATGCTTAAATAGTTGATGAA 120
  |||||
Db 61 atataatgacgtatgataaagtttaataactaccagatgcttcaaaaatagttgataa 120
QY 121 GATTTCAGCTTCCACCAAGGATTAATTCATGATTTAAACCCAGATTTATTTCTTT 180
  |||||
Db 121 gatttcagcttccacccatccatccatcgagaagttcttatcttaaaacttga 180
QY 181 CCACATCCAAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 240
  |||||
Db 181 ccacatccaaacataatgaatatttaagatgacttaaaatttgacgataatatta 240
QY 241 GTACCAAAATTTGATCGTATGATTTGATGATTTGATGATTTGATGATTTGATGATTTGAT 300
  |||||
Db 241 gtacccaatctgacgtatgataatgacgtatgataatgataatgataatgataatgataa 300
QY 301 CGAACAACACGATTTATTTATGTTATGTTATGTTATGTTATGTTATGTTATGTTATGTTAT 360
  |||||
Db 301 cgaacaacacgatttattatgattatgattatgattatgattatgattatgattatgattat 360
QY 361 GCTAATGAATTTGAAGAAAACATATCAATTAATGTTAAATCAATGATGATGATGATGAT 420
  |||||
Db 361 gctaatgaatctgagaagaaagatacaatattggttaaaatcaatgattcagactt 420
QY 421 GATTTATTCATTTCCACCAAGGATTAATTCATGATTTAAACCCAGATTTATTTCTTT 480
  |||||
Db 421 gatattatcatcacaagggataatcatcgtgataataaaccagtaattcttctt 480
QY 481 GCCCGGATGATTAACACACCGATTAATTTGAGATTTTGAATTTTGAATTTTGAATTTTGA 540
  |||||
Db 481 gcccggaatgataataacacacgattattggaatttggatattgattatgattataa 540
QY 541 CTGCCACCTAAAGATTAACCCCTATGCGGAATTAATTAATTAATTAATTAATTAATTAAT 600
  |||||
Db 541 ctgccacctaagaatgaaacccctatgcggaataatataatgataatgataatgataat 600
QY 601 AAAGCACCAGATTTGATTTGTTGTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 660
  |||||
Db 601 aaagcaccagatctgattcttggtataactaatatgaatgaatgaatgaatgaatgaat 660
QY 661 TTGGGTATTAATTTGACTGGTTTATATTCAGAAAATTTTCAAAAGTTTACTCAAAAGAT 720
  |||||
Db 661 ttgggtataatttgactggttataatcagaagaatcttcaagaagaatcttcaaatgaattgtagtg 720
```

Query Match	98.6%	Score 1004.6	DB 37	Length 1020
Best Local Similarity	99.1%	Pred. No. 2.3e-156		
Matches 1010	Conservative 0	Mismatches 9	Indels 0	Gaps 0
QY	1	ATGAAGTGTCTGAGATTATTATATATACACAGAAATTAATTACAACTAGTCGCAATTCCTGAT	60	
Db	1	atgaagttgttcgagattatataatagacaggaatlaattacaaatagtcgcaatttcgat	60	
QY	61	ATAATACGGCTATTTGATTAAGTTAAATTAACCTACCACTATGTCTTAATAATAGTTGATCAA	120	
Db	61	atatatacgcctatgataaagttlaataactaccagtagtcgtctaaatagttgatga	120	
QY	121	GATTTCAGGCTCCGCCGCACTTCAATCCATGAGCAAAATTTTAACTTAACCTTAAGTTGAA	180	
Db	121	gatttcaggtcttcaccacatccatccatccatccggaagttcctataccttaaaccttggaa	180	
QY	181	CCAGATCCAAACATTAATTTGAATATTTTAATGATCTTAAATTTATGATGATGTTATATTA	240	

```

RESULT      9
US-60-259-128-4099
: Sequence 4099, Application US/60259128
:
: GENERAL INFORMATION:
:
: APPLICANT: Roemer, Terry
:
: APPLICANT: Jiang, Bo
:
: APPLICANT: Boone, Charles
:
: APPLICANT: Bussey, Howard
:
: TITLE OF INVENTION: Gene Disruption Methodologies for Drug
:
: TITLE OF INVENTION: Target Discovery
:
: FILE REFERENCE: GRACE1
:
: CURRENT APPLICATION NUMBER: US/60/259,128
:
: CURRENT FILING DATE: 2000-12-29
:
: NUMBER OF SEQ ID NOS: 5129
:
: SOFTWARE: FastSeq for Windows Version 4.0
:
: SEQ ID NO 4099
:
: LENGTH: 1020
:
: TYPE: DNA

```

ORGANISM: Candida albicans
US-60-259-128-4099

```
Query Match          98.6%; Score 1004.6; DB 64; Length 1020;
Best Local Similarity 99.1%; Pred. No. 2.3e-156;
Matches 1010; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGAAGTTGTCAGATTATATATATAGACAAAGAAATTAATTTACAAATAGGCCATTTCTGAT 60
   |||||
DB 1 atgaagttgtcagattatataatagacaagaaatlaattacaaatagtgccatttcgatt 60

QY 61 ATATATACGGCTATTCATTAAGTTTAATACTACACAGATGTCTTAAATAAGTAGTGATAA 120
   |||||
DB 61 atataacggctatgataagtttaataacttaccagatagtccttaaaatagtgatgaa 120

QY 121 GATTTCAGTTCACACACATTCATTCACGAGAAATTTTATACCTTAAACTTTGAAA 180
   |||||
DB 121 gatttcagtctcaccacatccaatccatcgagaagttcctataacttaaaacttgaaa 180

QY 181 CCACATCCAAACATATATGATATTTTATGATCTTAAATTTATGATGATGTTATATTA 240
   |||||
DB 181 ccacatccaaacaataatgaaatatttlaaagatcttaaaatctgacgatattatla 240

QY 241 GTCACCAATTTGATGTTATGATTTGAGTCAATTCATTCATTCATTCATTCATTCAT 300
   |||||
DB 241 gtccaccaatttgatgcttattgattgattgagtcattgattgaaattacaataatctgtaa 300

QY 301 CGAACACACAGATTTTATGATGTTATTCGTAATCTTGTATGATATTCATTCATTCAT 360
   |||||
DB 301 cgaaacacacagatttatttattgattaaatggtlaaactctgttagtaataatacaact 360

QY 361 GCTAATGAAATTTGAAGAAAGATATCAATTCATTCATTCATTCATTCATTCATTCAT 420
   |||||
DB 361 gctaatgaaattgaaagaaagatacaaatatgattgaatcaatggtccagactt 420

QY 421 GAAATTTATTCATTCACACAGGATTAATTCATTCGATATATTAACCAAGTAATTTCTTT 480
   |||||
DB 421 gaatttatttcacacaaggataatcactggtatataaaacccaattatatttcttt 480

QY 481 GCCCGGATGATTAACACACAGGATTTATTCGATTTGATTTGATTTGATTTGATTTGATA 540
   |||||
DB 481 gcccggaatgataacaacacagattatgagatcttgatcttgtaaatgattaaaa 540

QY 541 CTCGCCACTTAAGATGAAACCCCTATGCGAAATATATTCATTCATTCATTCATTCAT 600
   |||||
DB 541 ctgcgcaacttaagatgaacccctatgsgaaatatattgattgattcctacagattat 600

QY 601 AAAGCACACAGATTCATTCGTTGATTAATTCATTCATTCATTCATTCATTCATTCAT 660
   |||||
DB 601 aaagcacacagatttcttggtataactaattatgaaatgaaatgataatcttgatca 660

QY 661 TTGGGATATTTTGAAGTGTATTCGAAATTTTCAAAATTTTCAAAATTTTCAAAATTT 720
   |||||
DB 661 ttgggatatatttgactggttataatctagaataattccaagtgctttagtccaagatt 720

QY 721 GATTAAGAAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 780
   |||||
DB 721 gataaagaatttgactaattgctcattgattgattatattatattacaataattt 780

QY 781 GAAAATTTGCGTACACCAATTTTAACTGATTTGAAGATGAATTTTGTGTGTAATAT 840
   |||||
DB 781 gaaaatttgcgtacaccatcttaactgatttgaagaatgaaatcttctgtgataat 840

QY 841 AATAATGAAATTCGATTTTAAATAATTCATTTTCAAAATTTTCAAAATTTTCAAAATTT 900
   |||||
DB 841 aataatgaaactgcattttaaataatcaattcaataataataatccctgaaagaattg 900

QY 901 GATATTTATTTACCTCGATGCAATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 960
   |||||
DB 901 gatattatttacctcgatgcaatgattgattcatgtaagaataattcttacaagaatgatt 960

QY 961 AGATATGATCGAAGTAAAGATTAACCTTAAAGAAATCTTACAAATTTATGTTGATG 1019
   |||||
```

```
DB 961 agatattgctgaagtgaaagaataacttcttaagaagaacttacaataatgattgattg 1019
   |||||

RESULT 10
US-60-314-050-6173
; Sequence 6173, Application US/60314050
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; APPLICANT: Ohlsen, Karl L.
; TITLE OF INVENTION: GENE DISRUPTION METHODOLOGIES FOR DRUG TARGET DISCOVERY
; FILE REFERENCE: 10182-013-888
; CURRENT APPLICATION NUMBER: US/60/314, 050
; NUMBER OF FILING DATE: 2001-08-22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6173
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Candida albicans
US-60-314-050-6173

Query Match          98.6%; Score 1004.6; DB 70; Length 1020;
Best Local Similarity 99.1%; Pred. No. 2.3e-156;
Matches 1010; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGAAGTTGTCAGATTATATATATAGACAAAGAAATTAATTTACAAATAGGCCATTTCTGAT 60
   |||||
DB 1 atgaagttgtcagattatataatagacaagaaatlaattacaaatagtgccatttcgatt 60

QY 61 ATATATACGGCTATTCATTAAGTTTAACTTACACAGATGTCTTAAATAAGTAGTGATAA 120
   |||||
DB 61 atataacggctatgataagtttaataacttaccagatagtccttaaaatagtgatgaa 120

QY 121 GATTTCAGTTCACACACATTCATTCACGAGAAATTTTATACCTTAAACTTTGAAA 180
   |||||
DB 121 gatttcagtctcaccacatccaatccatcgagaagttcctataacttaaaacttgaaa 180

QY 181 CCACATCCAAACATATATGATATTTTATGATCTTAAATTTATGATGATGTTATATTA 240
   |||||
DB 181 ccacatccaaacaataatgaaatatttlaaagatcttaaaatctgacgatattatla 240

QY 241 GTCACCAATTTGATGTTATGATTTGAGTCAATTCATTCATTCATTCATTCATTCAT 300
   |||||
DB 241 gtccaccaatttgatgcttattgattgattgagtcattgattgaaattacaataatctgtaa 300

QY 301 CGAACACACAGATTTATTCGTTGATTAATTCATTCATTCATTCATTCATTCATTCAT 360
   |||||
DB 301 cgaaacacacagatttatttattgattaaatggtlaaactctgttagtaataatacaact 360

QY 361 GCTAATGAAATTTGAAGAAAGATATCAATTCATTCATTCATTCATTCATTCATTCAT 420
   |||||
DB 361 gctaatgaaattgaaagaaagatacaaatatgattgaatcaatgaaatgaaatgaaatgaa 420

QY 421 GAAATTTATTCATTCACACAGGATTAATTCATTCGATATATTAACCAAGTAATTTCTTT 480
   |||||
DB 421 gaatttatttcacacaaggataatcactggtatataaaacccaattatatttcttt 480

QY 481 GCCCGGATGATTAACACACAGGATTTATTCGATTTGATTTGATTTGATTTGATTTGATA 540
   |||||
DB 481 gcccggaatgataacaacacagattatgagatcttgatattgattgattgatttataaa 540

QY 541 CTCGCCACTTAAGATGAAACCCCTATGCGAAATATATTCATTCATTCATTCATTCATTCAT 600
   |||||
DB 541 ctgcgcaacttaagatgaacccctatgsgaaatatattgattgattcctacagattat 600

QY 601 AAAGCACACAGATTCATTCGTTGATTAATTCATTCATTCATTCATTCATTCATTCATTCAT 660
   |||||
DB 601 aaagcacacagatttcttggtataactaattatgaaatgaaatgataatgattgattgca 660
```

```
QY 661 TTGGGTAATATTTTGAAGTGGTTATATTCAGAAAATTTTCAAGTGTCTTGTAGTCAAGAT 720
      |||
Db 661 ttgggataatttgcattggttatattcagaagaatttccaagtgctttaglcaaagat 720
QY 721 GATTAAGAAATGCTATATATCTCATGTGTAGTATTAATTAATCAAAATATTT 780
      |||
Db 721 gataaagaattgactaattctcattgtagttagtattatatttaataccaatattt 780
QY 781 GAAATTTGGGTACACCCATTTAACTGATTTTGAAGATGATTTTGTGATGAATAT 840
      |||
Db 781 gaaaatttgcgaaccacatttaactgatttgaagaatattcttgtagaataat 840
QY 841 AATTAATGAAACTTGCTATTTTAAAAATTCATTTACAAAATATCTGAGAAAGATTGG 900
      |||
Db 841 aataaagaacttgctattttaaaaaattccaatttcaaaaatctccagaagaattgg 900
QY 901 GATATATTTTACCTCGATGCAATGATGATTTAATGAAGAAATTTTACCAAGATGATT 960
      |||
Db 901 gataattattcactcgatgcaatgataattcatgaaagaatttaccagaatgatt 960
QY 961 AGATATGATGCAAGTAAGAAAGATTAATCTTAAGAAATCTTCAATTAATGTTGATTGG 1019
      |||
Db 961 agatattgacgaagaagaataaacttctaagaagaattcctaataatgtagattg 1019
```

```
RESULT 11
US-09-248-796-4351
; Sequence 4351, Application US/09248796
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248.796
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 28206
; SEQ ID NO 4351
; LENGTH: 1038
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796-4351
```

Query Match 98.4%; Score 1003; DB 16; Length 1038;
Best Local Similarity 99.0%; Pred. No. 4.3e-156;
Matches 1009; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```
QY 1 ATGAAGTTGTCAGATTATTTATATAGCAAGAAATTAATTTCAATAGTCCGATTTGCAT 60
      |||
Db 19 atgaagttgtcagattatattatataagcaagaatlaaattacaatagtgccatttcgat 78
QY 61 ATATATACGGCTATTGATTAAGTTTAATTAACCTTACCGAGTAGTGTCTTAATAATAGTTGANGAA 120
      |||
Db 79 atataacggtcattgtaagttlaaacttaactaccagatgcttctaaataatgttgagaa 138
QY 121 GATTTCAGCTCTCCACCATTTCAATCCATCGAGAAATTTTATTACTTAAACTTTGAAA 180
      |||
Db 139 gatttcagctctccaccatctcaatccatcgcagagatctctataacttaaaacttggaa 198
QY 181 CCACATCCAAACATTAATTAATTAATTAATGATCTTAATAATTTTANGATGCTTATATTTA 240
      |||
Db 199 coactccaaaacataatgataatttcaatgacttcaaaaatttgcagataattatata 258
QY 241 CTCACCAAAATTTGATCGTTATGATTTGAGTCAATTTGATTTGAATAATTTGTAAA 300
      |||
Db 259 gtcccaaatgtcatcgtatgattgagtcacattgattgaattacaataatgtgtaa 318
QY 301 CGAACCAACAGATTATTTATGATTAATGATTAATGTAATCTTGTACTAATCAATATACACTT 360
      |||
Db 319 cgaacaaacagattatattatcgtatcaatgtaactctgtagtaatacatatacactt 378
QY 361 GCTAATGAATTAAGAAAAGAAATGATATCAATTAATGTTAAATCAATGAGTTCGAGACTT 420
```

```
Db 379 gctaatgaaattgagaagaatacatcaactatcgttlaaaatloaatgagtlcaggactt 438
QY 421 GAATTTATTCATTCACAAGGGATTAATTCATCGTATATTAACCAAGTAAATTTTGTCTT 480
      |||
Db 439 gaatttattcattccaaggataattcattcatcgtgataataaacccagtaattatttcttc 438
QY 481 GCCCGGATGATTAATTAACCAACCCGATTAATTTGAGATTTTGTATTTGTATTTAAA 540
      |||
Db 499 gcccggaatgataacaacaacgattatggagatttggatttltatgtattttaa 558
QY 541 CTGCCACCTAAGATGAACCCCTATGCGCAATATTAATGATGATTAATGATTAATTTAT 600
      |||
Db 559 ctgcacactaaagtgtgaacccccctatggcgaaatattgatactcaccaggtattat 618
QY 601 AAAGCACCAGAAATTTGATTTTGTATTAATTAATTAATTAATTAATTTGATTTGTCGA 660
      |||
Db 619 aaagcaccagaattgattcttgtagataactaatatgaaatgaaattgatttggtaa 678
QY 661 TTGGGTAATATTTGACGTGTTTATTCAGAAAATTTTCAAGTGTCTTGTAGTCAAGAT 720
      |||
Db 679 ttgggataatttgcattggttatattcagaagaatttccaagtgctttaglcaaagat 738
QY 721 GATTAAGAAATTTGACTAATGATTTCTCATGTGTAGTATTAATTAATTAATTAATTT 780
      |||
Db 739 gataaagaattgactaattgattcctcattgtagttagtattatatttaataccaatatt 798
QY 781 GAAATTTGGGTACACCCATTTAACTGATTTTGAAGATGATTTTGTGATGAATAT 840
      |||
Db 799 gaaaatttgcgaaccacatttaactgatttgaagatgaaattatttgcgtgaatat 858
QY 841 AATTAAGAAACTTGCTATTTTAAAAATTCATTTTCAAAAATATCTGAGAAAGATTGG 900
      |||
Db 859 aataatgaaaacttgactgctttaaataatlaacttaacaaaataccctagaagatgg 918
QY 901 GATATTTTACCTCGATGCAATGATGATTTAATGAAGAAATTTTACCAAGATGATT 960
      |||
Db 919 gataattattcactcgatgcaatgataattcatgaaagataatttaccagaatgatt 978
QY 961 AGATATGATGCAAGTAAGAAAGATTAATCTTAAGAAATCTTCAATTAATTAATGTTGATTGG 1019
      |||
Db 979 agataatgacgaagtttcaagaataaacttcaagaagaattcctaataatgtagattg 1037
```

```
RESULT 12
US-60-096-409-4351
; Sequence 4351, Application US/60096409A
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBI
; FILE REFERENCE: GTC-016P
; CURRENT APPLICATION NUMBER: US/60/096.409A
; CURRENT FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28206
; SEQ ID NO 4351
; LENGTH: 1038
; TYPE: DNA
; ORGANISM: Candida albicans
US-60-096-409-4351
```

Query Match 98.4%; Score 1003; DB 48; Length 1038;
Best Local Similarity 99.0%; Pred. No. 4.3e-156;
Matches 1009; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```
QY 1 ATGAAGTTGTCAGATTATTTATATAGCAAGAAATTAATTTCAATAGTCCGATTTGCAT 60
      |||
Db 19 atgaagttgtcagattatattatataagcaagaatlaaacttaataatgtagtcatttcgat 78
QY 61 ATATATACGGCTATTGATTAAGTTTAATTAACCTTACCGAGTAGTGTCTTAATAATAGTTGANGAA 120
      |||
Db 79 atataacggtcattgtaagttlaaacttaaccagatgcttcaaaaatgtagtgaa 138
```



```
Db      181  |||tttcggtacaccacatttaacgatttgaagatgagattatttctgtagtaataataa 240
QY      846  |||TGAACCTTGCAATTTAAAAA 867
Db      241  |||tgaacttgcattttaaaaa 262
```

RESULT 15

```
US-60-127-461-6591
; Sequence 6591, Application US/60127461
; GENERAL INFORMATION:
; APPLICANT: Chapman, Rowan
; APPLICANT: Thornton, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF CANDIDA ALBICANS
; FILE REFERENCE: PM-0007-2 P
; CURRENT APPLICATION NUMBER: US/60/127,461
; NUMBER OF SEQ ID NOS: 8247
; SOFTWARE: PERL Program
; SEQ ID NO 6591
; LENGTH: 260
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: _
; OTHER INFORMATION: ATFB08591828
US-60-127-461-6591
```

```
Query Match      25.3%; Score 258; DB 51; Length 260;
Best Local Similarity 100.0%; Pred. No. 3,6e-33;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      492  TATAACACACCGATTATTTGAGATTTTGTATGATTTAAAGTCCACCTAA 551
Db      1    tataacacacccgattatttgagatttgatattgtaataaactgcacccaa 60
QY      552  AGATGACCCCTATAGCGGAATATATGATGTATCTACAGGTATTTAAAGCACGAGA 611
Db      61  agatgaacccctatgcgaaatatatgatactacaggtattataaagcacccaga 120
QY      612  ATTGATTCCTGGTATACATTAATTAATGAAATGATGATTTGGTCATTTGGGTATAT 671
Db      121  attgattcttggtaataactaataatgaataatgaataatcgtgcatcgggtataat 180
QY      672  TTGACTGGTTATATTCAGAAAATTTCAAGTGTTTAGTCAAGATGATAAGAAAT 731
Db      181  ttgacttggttataatcagaaaatttcaaagtgtttagtcaaagtgaataaagaatt 240
QY      732  GACTAATGATTCTCATGT 749
Db      241  gactaatgattcctcatgt 258
```

Search completed: May 29, 2002, 14:50:37
Job time: 17726 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2002, 09:55:12 ; Search time 66.37 Seconds
(without alignments)
3771.290 Million cell updates/sec

Title: US-09-072-994A-13

Perfect score: 1019
Sequence: 1 ATGAAGTTGCAGATTATTA.....TTACATTATTAATTGATG 1019

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/lna/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/lna/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/lna/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/lna/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/lna/PCURS.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61.8	6.1	615	4	US-08-998-416-186
2	59.6	5.8	1431	4	US-09-316-083-2
3	59.4	5.8	828	4	US-08-998-416-538
4	59	5.8	834	4	US-08-998-416-305
5	58.6	5.8	665	2	US-08-883-795A-36
6	58.2	5.7	665	2	US-08-883-795A-36
7	58.2	5.7	19124	2	US-08-487-826B-13
8	57	5.6	636	4	US-08-998-416-1137
9	56.2	5.5	8920	2	US-08-446-855A-1
10	56.2	5.5	8920	4	US-09-150-741-1
11	54.4	5.3	767	4	US-08-998-416-472
12	53.8	5.3	724	4	US-08-998-416-683
13	53.8	5.3	854	4	US-08-998-416-534
14	53.8	5.3	860	4	US-08-998-416-287
15	53.6	5.3	837	4	US-08-998-416-288
16	53.4	5.2	663	4	US-08-998-416-191
17	53.4	5.2	19124	2	US-08-487-826B-13
18	53	5.2	1070	1	US-08-463-090B-5
19	52	5.1	837	4	US-08-998-416-288
20	51.8	5.1	51952	3	US-08-947-823-1
21	51.4	5.0	2483	3	US-08-526-964-1
22	51.4	5.0	2483	2	US-08-946-617-1
23	51.4	5.0	2483	3	US-09-031-897-1
24	51.4	5.0	5203	4	US-09-027-770-1
25	50.8	5.0	1431	4	US-09-316-083-2
26	50.6	5.0	615	4	US-08-998-416-186
27	50.6	5.0	724	4	US-08-998-416-683

C 28	50.6	5.0	6124	4	US-08-213-419B-3	Sequence 3, Appl
C 29	50.4	4.9	711	4	US-08-998-416-786	Sequence 786, App
C 30	50.4	4.9	2317	3	US-08-749-522-5	Sequence 5, Appl
C 31	50.4	4.9	3974	4	US-08-467-504-3	Sequence 3, Appl
C 32	50.4	4.9	6124	4	US-08-213-419B-3	Sequence 3, Appl
C 33	50.4	4.9	8920	2	US-08-446-855A-1	Sequence 1, Appl
C 34	50.4	4.9	8920	4	US-09-150-741-1	Sequence 1, Appl
C 35	50.2	4.9	662	4	US-08-998-416-185	Sequence 185, App
C 36	50.2	4.9	665	4	US-08-998-416-937	Sequence 937, App
C 37	50.2	4.9	732	4	US-08-998-416-1036	Sequence 1036, App
C 38	50	4.9	701	4	US-08-998-416-701	Sequence 701, App
C 39	50	4.9	854	4	US-08-998-416-534	Sequence 534, App
C 40	49	4.8	1511	1	US-07-991-867B-8	Sequence 8, Appl
C 41	49	4.8	1511	1	US-08-107-755A-8	Sequence 8, Appl
C 42	49	4.8	1511	2	US-08-544-332-8	Sequence 8, Appl
C 43	48.8	4.8	636	4	US-08-998-416-1137	Sequence 1137, App
C 44	48.8	4.8	827	4	US-08-998-416-535	Sequence 535, App
C 45	48.8	4.8	1395	1	US-07-991-867B-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-08-998-416-186/c
Sequence 186, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippesen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Redlschunz, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1074RP

TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 538:
SEQUENCE CHARACTERISTICS:
LENGTH: 828 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1375RP
US-08-998-416-538

Query Match 5.8%; Score 59.4; DB 4; Length 828;
Best Local Similarity 48.8%; Pred. No. 0.00063;
Matches 191; Conservative 0; Mismatches 196; Indels 4; Gaps 1;
QY 632 ATTATGAAATGAAATGTAATTTGGTCAATTTGGTATTAATTTTGACTGGTTATATTCAG 691
DB 692 ATATATTAATTAATAATTTACCATTTAATGATATATTTATCAAAAAATTAATGTTATA 633
QY 692 AAAATTTCAAGTGTAGTCAAAAGATGAATGAATGACTATGATTCATGTTA 751
DB 632 AAATTAATTAATTAATTTACTAATTAATTAATTAATTAATTAATTAATTAATTA 573
QY 752 GTGATTTATATTTATTAATCAAAATTTGAAATTTTGGTACACCAATTTAACTGATT 811
DB 572 TTAATTTATATCTTAGTATTAATTAATTTAGATTAGTTCTTATATATATATATAT 513
QY 812 TTGAAGTAAATTAATTTTGTGATGA---ATATTAATGAAGAACTTGCAATTTAAAAA 867
DB 512 TAGGTAAATTTAGTAGTAAATTAATCAATTAAGGTAGACTATTAATTAAGAAATA 453
QY 868 TTCAATTTCAAAAATATCTAGAAAAGTTGGGATTTATTTTACCCTGATGCAATAT 927
DB 452 TTCTAGACTAATTAATAATTAATTAATGAAGGTACATTTTAATTAATTAATTAATCA 393
QY 928 GATTTAATGAAGAAATTTTACCAAGATGATTAATGATGCAAGTAAAGAAATTAAT 987
DB 392 GAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 333
QY 988 TCTAAGAAATCTTCAATTAATTTGATTT 1018
DB 332 ATATCTATTTTATTAATTAATAAAGTGTATATT 302

RESULT 4
US-08-998-416-305/c
Sequence 305; Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Reibischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPTII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 305:
SEQUENCE CHARACTERISTICS:
LENGTH: 834 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1250RP
US-08-998-416-305

Query Match 5.8%; Score 59; DB 4; Length 834;
Best Local Similarity 48.8%; Pred. No. 0.00075;
Matches 190; Conservative 0; Mismatches 195; Indels 4; Gaps 1;
QY 634 TATGATATGAAATGTAATTTGGTCAATTTGGTATTAATTTTGACTGGTTATATTCAGAA 693
DB 689 TATTAATTAATTAATTTACCATTTAATGATTAATTAATTAATTAATTAATTAATTA 630
QY 694 AATTTTCAAGGTGTTTACCAAGATGAATGAATGACTAATGATTCATGTTAGT 753
DB 629 AATTAATTAATTAATTTACTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 570
QY 754 GATTTATATTTATTAATCAAAATTTGAAATTTTGGTACACCAATTTAACTGATTTT 813
DB 569 AATTAATTAATCTTAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 510
QY 814 GAAGATGAATTAATTTTGTGATGA---ATATTAATGAAGAACTTGCAATTTAAAAAAT 869
DB 509 GTTAATTAATTTAGTAGTAAATTAATCAATTAAGGTAGACTATTAATTAAGAAATATT 450

Db 6421 ATTATATAAAAGCTTTTATCATCTTTGTTGTGATTTTATGATTTTCATGCATTT 6362
QY 832 GATGATATATATATGAAAGCTTCATTTTAAATAATTCATTTCAAAAATATCTTGA 891
Db 6361 TATGATTTTCAAAATTTTATGATTAATATAAATAAATAAATACATTAATAAA 6302
QY 892 AAGATTTGGATATATTTTACCTGATGCATGATGATTAATGAAGAATTTTATAC 951
Db 6301 TATATATATTCATTAATATGAGTTATTAATTAATGTTCTATGTTATATATTAAT 6242
QY 952 AAGATGATTAATGATGAGTGAAGTAAAGATTAATCTTAAAGAAATCTTCAATTAATG 1011
Db 6241 GAAATATTTGTTATATATATTAATATACATATAT- GCTACTATATAAATATTAATATCT 6183
QY 1012 TTGGAT 1018
Db 6182 TTAAAGT 6176

RESULT 8

US-08-998-416-1137/C
Sequence 1137, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jürgen
APPLICANT: Knechtle, Philipp
APPLICANT: Redlschunig, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSEYII
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ. ID NO: 1137:
SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1692RP
US-08-998-416-1137

Query Match

5.6%; Score 57; DB 4; Length 636;

Best Local Similarity 43.4%; Pred. No. 0.0018;
Matches 261; Conservative 0; Mismatches 340; Indels 0; Gaps 0;

QY 273 ATTGATTTGAATATACAAATATTTGTAAACGACACACGATTTATTTATGATTAATACG 332
Db 602 ATTTTATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 543
QY 333 TAATCTTGTAGTAATCAATATATACCTGCTAATGAAATTTGAAGAAAAGATATCAAT 392
Db 542 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 483
QY 393 ATGTTAAATCAATGAGTTGAGCTTGAATTTATTCATTCACAAGGATATATTCACG 452
Db 482 AAGTTAAATTAATTTTATTAATTAATTTCTTATTAAGAAATTAATTAATTAATTAACGA 423
QY 453 TGATTAAGCCAGTAATATTTTCTTGCCCGGATGATATACACACGATTAATGG 512
Db 422 TAATATTTAATAAATAGATATTAATTAATAAATAATTAATTAATTAATTAATTAAT 363
QY 513 AGATTTGATTTGTTATGATTTAAACTGCCACTAAGATGAACCCCTATGGCGGA 572
Db 362 AATCTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 303
QY 573 ATATATGATGTATCTACAGTATTTATAAGCAGCAAGATGATCTTGATTAATCTAA 632
Db 302 TATGATTAATCTATTTAATTAATTTAAGAAATTAATTAATTAATTAATTAATTTAAT 243
QY 633 TTATGATATGAAATGATATTTGTCATGCTATGATTAATTTGATGTTATTAATTCAGA 692
Db 242 AACTAATTTAAATTTGAACATGACATAATTAATTAATTAATTAATTAATTAATTAAT 183
QY 693 AAATTTCAAGCTTTTATGCAAGATGATAAGATTAAGATTAATTAATTAATTAATTAAT 752
Db 182 TTATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 123
QY 753 TGATTTATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 812
Db 122 TAATTAATCAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 63
QY 813 TGAAGATGAATTAATTTGTGATGAATTAATTAATTAATTAATTAATTAATTAATTAAT 872
Db 62 TAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3
QY 873 T 873
Db 2 T 2

RESULT 9

US-08-446-855A-1
Sequence 1, Application US/08446855A
Patent No. 5849573
GENERAL INFORMATION:
APPLICANT: Stewart, Thomas S
APPLICANT: Flores, Maria V
APPLICANT: O'Sullivan, William J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 1100 No. 5849573th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,855A

```

: FILING DATE: 06-Jul-1995
:
: CLASSIFICATION: 435
:
: ATTORNEY/AGENT INFORMATION:
:
:   NAME: Mltchard, Leonard C
:   REGISTRATION NUMBER: 29,009
:
: REFERENCE/DOCKET NUMBER: 47-80
:
: TELECOMMUNICATION INFORMATION:
:
:   TELEPHONE: 703-816-4000
:
:   TELEFAX: 703-816-4100
:
: INFORMATION FOR SEQ ID NO: 1:
:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 8920 base pairs
:     TYPE: nucleic acid
:     STRANDEDNESS: single
:     TOPOLOGY: linear
:
:   MOLECULE TYPE: genomic
:
: OS-08-446-855A-1

```

Query Match	5.5%;	Score 56.2;	DB 2;	Length 8920;
Best Local Similarity	45.4%;	Pred. No. 0.0037;		
Matches 328; Conservative	0;	Mismatches 383;	Indels 12;	Gaps 3

QY	153	AGAAATTTTATCTTAAACCTTGAAACACATCCAAACATATTTGAATATTTAATGA	212
Db	5854	AGGGAATATATAAAAATATGATATGTATTTATCTAAGAAAAAGATATCTTAAATAAAA	5913
QY	213	TCCTTAAATTTATGATGATGTATTAATTATAGCCAAATGTATCGTTATGATTGAGTCA	272
Db	5914	CCCTGTAATTTCTTATATGTTGTACATTCCTGATATATATATGATATCCAAATTAATA	5973
QY	273	ATTGATTTGAATTTACAAATATTTGTAAACGAACACAGATTTATTTATGTTAATATGG	332
Db	5974	GATGAAGAAGATTATATGATATACGAAATTTAAATGATGATATTAATATATGTTAAAT	6033
QY	333	TAATCTTGTAGTAACCAATATACACTCTCTATGAAATG-----AAGAAAAAGAT	384
Db	6034	GAATGTGTCAATATTAATATATGCTAGTGCATTTGTAATGSAAGATAGAAATGATTA	6093
QY	385	ATCAAAATATGTTTAAATCAATGACTTCAGA-CTTGAAATTTATTCATCAACAGGAT	443
Db	6094	TTTAGAAAAATGATTTGATTGAAAAAAATATGGATCATACATACAAACATTTAATATGTTT	6153
QY	444	ATTTCATCGGATATTAACCAACCAAGTAAATTTTCTTGGCCGGGTGATATPACACAAC	503
Db	6154	AAACAATCGTAGACATACAAATGAGAGGTATGCTTATGTAAACAATGAAAAAGAG	6213
QY	504	GATTATTTGAGATTTTGGATTTTGGTATTTTAAACCTGCACCTTAAGATGACCCCC	563
Db	6214	CATTCATGAGAGGCCCATAGAAAGAAATGCTTTAAATATAAAAAATTAAGAAAA---AA	6270
QY	564	TATGGCGAAATATTTGATGTATCTPACAGTATTTTATPAAAGCACCAGATTTGATCTTGG	623
Db	6271	TATGAAAAAAATTAAGGAAAAAATTAAGACAAAAAGAAATATCATTTTGTATTCATTA	6330
QY	624	TATTACTAATTTATGAAATATGAATTAATTTGTCATTTGGGTAAATTTGACTGCTT	683
Db	6331	AAGGATTAATGATATATATAGTAAACAATATTTGATCGAAGTTTATATATTAATTAATGTTGATGA	6390
QY	684	ATATTCAGAAAAATTTTCAAAGTGTTTAGTCAAAAGATATTAAGAAATATGACTAATGATTC	743
Db	6391	TATTAATTAATAAAGATATATTAAGAGATGAAGAAATGATATATATTAATTTACACTTGTCT	6450
QY	744	TCATGTTACTGATTAATATTTATTTAAATCAAAATATTTTAAAAATTTCCGTACACCCAATTT	803
Db	6451	ACAGGTAAACAATGACGATTTAAGTAAGATAATTAATTAATTTAAGTGTGAGTAAGATTAAC	6510
QY	804	AACTGATTTTGAGAGATGAAATTTTGTGATGAATATATATATGAAGAACTGGCATTTTAA	863
Db	6511	TGATGTGATATGATGATTAATTAATATGATGAAGATGAAGAGATGACTATGACGATGA	6570
QY	864	AAA 866	

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      DB      6571 TAA 6573

      RESULT 10
      US-09-150-741-1
      ; Sequence 1, Application US/09150741
      ; Patent No. 6183996
      ; GENERAL INFORMATION:
      ; APPLICANT: Stewart et al.
      ; TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
      ; Patent No. 6183996
      ; TITLE OF INVENTION: Synthetase II
      ; FILE REFERENCE:
      ; CURRENT APPLICATION NUMBER: US/09/150,741
      ; CURRENT FILING DATE: 1998-09-10
      ; EARLIER APPLICATION NUMBER: PL6880
      ; EARLIER FILING DATE: 1992-12-16
      ; EARLIER APPLICATION NUMBER: AU93/00617
      ; EARLIER FILING DATE: 1993-12-02
      ; EARLIER APPLICATION NUMBER: 08/446,855
      ; EARLIER FILING DATE: 1995-07-06
      ; NUMBER OF SEQ ID NOS: 15
      ; SOFTWARE: Patentln Ver. 2.0
      SEQ ID NO 1
      ;
      ; LENGTH: 8920
      ;
      ; TYPE: DNA
      ; ORGANISM: Plasmodium falciparum
      US-09-150-741-1

```

Query Match	5.5%;	Score 56.2;	DB 4;	Length 8920;
Best Local Similarity	45.4%;	Pred. No. 0.0037;		
Matches 328; Conservative	0;	Mismatches 383;	Indels 12;	Gaps 3

QY	153	AGAAATTTTCTACTTAAACCTTGGAAACACACATCCAAACATATATGAATTTTAAATA	212
Db	5854	agggaaataaataaataatgatalgtaattctatctaaggaaaaagatatacttaataaaa	591:
QY	213	TCTTAAATTTTANTCATGTATATATAGCACCAAAATTGTATCGTTATGATTTGGTGA	272
Db	5914	cccgtaattcttatttaigtltgtagctccgatatataatgaaacaaaattaataa	5977:
QY	273	ATTGATTGAAATTACAAATATTTGTAAACGACACACAGATTATTTTATGTATTAATG	332
Db	5974	gatgaagagfltaatagatacgaaaatttaaatgtatataataataatgaatgaataa	6033:
QY	333	TAACTCTGTAGTATACATATATACACTTGCTAATGAAATG-----AAAGAAAAGAT	384
Db	6034	gaattgttcttaataataataatgctagtgatttgttaaaatggaagatagaatgataa	6093:
QY	385	ATCAAAATATGTGTAAATATCAATGAGTGCAGCA-CTTGAAATTTATTCATTCACAAGGAT	443
Db	6094	tttagaaataatgattgtcataatgaaaaaataatgatactacatacaaacattataacgltt	6155:
QY	444	AATTCACTGTGATATAAAACCCAGTAAATATTTCTTTGCCGGGATGATATTAACAAC	503
Db	6154	aaacaactcglagaagtaacaatgagsgatgcttagtgytaaacaaatgaaaagaagag	6213:
QY	504	GATTATTTGGAGATTTTGATATTTTGTATATGTTTTAAACTGCCACCTAAAGATGAACCCC	563
Db	6214	caactcagaaagggccatcagaagaattggtttaaaataaaaaataagaaaaaa--aa	6270:
QY	564	TATGGCCAATATATTTGATGTATCTCCAGGTATTTATAAGCACAGAAATGATCTTGG	623
Db	6271	taaggaataaaataaagggaataaataaagaacaaataaataatcatctatgttaatacaaa	6330:
QY	624	TATTAATTAATTAATGAATGAATGAATTTGTCATTTGGGTAAATTTTACATCGCTTT	683
Db	6331	aaggaaataatgaataatgaatgaataacatatgaatcogaagtttaataatattgttgatga	6390:
QY	684	ATATTTCAGAAATTTTCAAAGCTGTTTTACTCAAAGATGATTAAGAATTGACTTAATGATTC	743
Db	6391	tataaataaataaagaatataatgaagaataaataatataatatttttttgaacatctgc	6450:

QY	744	TCAGTTAGGATTTATATATTTATTAATCAATCAATTTGGAATCCCAATTT	803
Db	6451	acaaggtacaacatgagcagatttaagtaatgaatbatttaagtaagtaagaattgaatc	6510
QY	804	AACGATTTTGAAGTGAATTTTGTGATGCAATTAATTAATGAAACTTCATTTTAA	863
Db	6511	tgtatgataatgatagatattattattattatcatgatgaagtgaagaagatgactatgaacatga	6570
QY	864	AAA	866
Db	6571	taa	6573

RESULT 11
US-08-998-416-472/c
; Sequence 472, Application US/08998416
; Patent No. 6239264
SEQUENCE INFORMATION

1. CONTACT:
 2. APPLICANT: Philipsen, Peter
 3. APPLICANT: Pohlmann, Rainer
 4. APPLICANT: Steinert, Sabine
 5. APPLICANT: Mohr, Christine
 6. APPLICANT: Wendland, Jurgen
 7. APPLICANT: Knechtle, Philipp
 8. APPLICANT: Reibschunung, Corinne
 9. TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPII
 10. TITLE OF INVENTION: AND USES THEREOF
 11. NUMBER OF SEQUENCES: 1152
 12. CORRESPONDENCE ADDRESS:
 13.
 14.
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ADDRESS: No.6239264rtlis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709

1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: Floppy disk
3 COMPUTER: IBM PC compatible
4 OPERATING SYSTEM: PC-DOS/MS-DOS
5 SOFTWARE: PatentIn Release #1.0, Version #1.30
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/08/998,416
8 FILING DATE: 24-DEC-1997

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 472:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 767 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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US-08-998-416-472
; ORGANISM: PAG1337RP
; ORIGINAL SOURCE:

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Similarity	45.78	Pred. No. 0.0061		
Best Local				
Matches 225	Conservative	0	Mismatches 266	Indels 1
				Gaps 1

QY 499 CAACCGATTATGGAGATTTTCATATTGTTATGATTTAAACACTGCCACCCTAAGAATGAA 588
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D	b	651	CAAAAAATTGTGTAATAAAAAAATAATATATATTTACTATTAATAAATTTAAAT	592
O	y	559	CCCCATGCGCAAAATATTTGATGCTATCTACAGGTATTTATAAGCACCAGAAATTGAT	618
D	b	591	ATAATATAAAAAAGATTAATTAATTTATATACCTTAGATPAATTAATTTAGATTTAAG	532
O	y	619	CTGGTATTAACATATTTATGATATGAATGATATTTGGTCATTTGGGTAAATTTTGACT	678
D	b	531	TATCTTAATATATATTTATAGTAATATTTTNGTNGTAATATATCCAAATTAAGG	472
O	y	679	GGTTATATTCAGAAATTTTCAAGTGTTTACTCAAAGATGATAAGAAATTGACTAAT	738
D	b	471	AGACATTAATTAATAGAAATTTCTAGACTATAAAAAATAATATTAAGAAAGGTCA	412
O	y	739	GATTCCTGTTAGATTTTATTTATTAATCAAAATATTTGCAAAATTTGCGTACACC	798
D	b	411	ATAATTTATATATCATGATGAAGTAATTAATTAATTAATTAATTAATTTATATCA	352
O	y	799	AATTTACTGATTTTGAGATGAAATTTTGTGTGATGATATTAATAATGAAAACCTTCA	857
D	b	351	CTTATATTAATAAACCTTAATATCTATTTTATTAATAAAATGTAATTTTAATTTAAA	292
O	y	858	TTTTAAAAAATTCATTTACAAAAATATCTCAGAAAGATGGAGATTTATTTTACCTCG	917
D	b	291	ATTAATTTAATACATTTTAATAATATCTATAGAAATTTCTATTATTTTATACA	232
O	y	918	ATGCAATGATGTTTAAATGAAAGAAATTTTACCAAGATGATTGATATGATCGAAGTAA	977
D	b	231	TTTTTAAATGTTTTTGTTAATGATATATATCAATTAATTAATTAATAAATTAAGATGCC	172
O	y	978	AAGATTAACCTC	989
D	b	171	ACAAATTAATTC	160

RESULT 12
US-08-998-416-683/c
; Sequence 683, Application US/08998416
; Patent No. 6239264
GENERAL INFORMATION:

```

1
2
3 GENERAL INFORMATION:
4 APPLICANT: Philippsen, Peter
5 APPLICANT: Pohlmann, Rainer
6 APPLICANT: Stehner, Sabine
7 APPLICANT: Mohr, Christine
8 APPLICANT: Wendland, Jürgen
9 APPLICANT: Knechtle, Philipp
10 APPLICANT: Reibschung, Corinne
11 TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPII
12 TITLE OF INVENTION: AND USES THEREOF
13
14 NUMBER OF SEQUENCES: 1152
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16 CORRESPONDENCE ADDRESS:
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ADDRESS: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA

```

1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Floppy disk
3  COMPUTER: IBM PC compatible
4  OPERATING SYSTEM: PC-DOS/MS-DOS
5  SOFTWARE: PatentIn Release #1.0, Version #1.30
6  CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976

ADDRESS: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
City: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

APPLICANT: Philippssen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jürgen
APPLICANT: Knechtle, Philipp
APPLICANT: Reibischung, Corinna


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QY 446 TTCATCGATATAAACCAGTAATATTTCTTGGCCGGAGATATATACACACGA 505
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Search completed: May 29, 2002, 14:52:06
Job time: 17814 sec

GenCore version 4.5
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OK protein - protein search, using sw model

Run on: May 29, 2002, 09:58:57 ; Search time 12.26 Seconds
(without alignments)
790.728 Million cell updates/sec

Title: US-09-072-994A-14
Perfect score: 1791
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 118494 seqs, 28596836 residues

Total number of hits satisfying chosen parameters: 118494

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	262	14.6	7	US-60-366-892-7 Sequence 7, App1
3	256	14.3	7	US-60-366-892-8 Sequence 8, App1
4	255.5	14.3	7	US-60-366-892-39 Sequence 39, App1
5	253.5	14.2	5	US-09-863-776-40 Sequence 40, App1
6	249	13.9	7	US-60-370-796-7 Sequence 7, App1
7	240.5	13.4	7	US-60-366-892-6 Sequence 6, App1
8	236.5	13.2	7	US-60-366-892-38 Sequence 38, App1
9	235	13.1	7	US-60-366-892-43 Sequence 43, App1
10	235	13.1	5	US-09-909-650A-24 Sequence 24, App1
11	235	13.1	7	US-60-366-892-40 Sequence 40, App1
12	232	13.0	4	US-09-573-655B-1255 Sequence 1255, App1
13	224.5	12.5	3	PCT-US02-13142-8265 Sequence 8265, App1
14	224.5	12.5	6	US-10-128-714-8265 Sequence 8265, App1
15	224.5	12.5	6	US-10-102-806-490 Sequence 490, App1
16	224	12.5	7	US-60-366-892-24 Sequence 24, App1
17	222.5	12.4	4	PCT-US02-13142-8141 Sequence 8141, App1
18	222.5	12.4	4	US-10-128-714-8141 Sequence 8141, App1
19	221.5	12.4	7	US-09-863-776-41 Sequence 41, App1
20	221.5	12.4	7	US-60-366-892-12 Sequence 12, App1
21	220	12.3	9	PCT-US02-13142-3141 Sequence 3141, App1
22	220	12.3	6	US-10-128-714-3141 Sequence 3141, App1
23	220	12.3	3	US-09-573-655B-1256 Sequence 1256, App1
24	218	12.2	5	US-09-393-212-8 Sequence 8, App1
25	218	12.2	7	US-60-366-892-19 Sequence 19, App1
26	218	12.2	5	US-09-393-212-2 Sequence 2, App1

27	218	12.2	404	5	US-09-393-212-7	Sequence 7, App1
28	216	12.1	815	7	US-60-366-892-23	Sequence 23, App1
29	215	12.0	360	7	US-60-366-892-20	Sequence 20, App1
30	215	12.0	380	5	US-09-393-212-9	Sequence 9, App1
31	215	12.0	721	7	US-60-366-892-21	Sequence 21, App1
32	213.5	11.9	464	7	US-60-366-892-13	Sequence 13, App1
33	211.5	11.8	250	5	US-09-718-032-5	Sequence 5, App1
34	209.5	11.7	268	6	PCT-US02-13142-3265	Sequence 3265, App1
35	209.5	11.7	268	6	US-10-128-714-3265	Sequence 3265, App1
36	206	11.5	557	7	US-60-366-892-22	Sequence 22, App1
37	206	11.5	557	7	US-09-393-212-10	Sequence 10, App1
38	206	11.5	587	1	PCT-US02-10818-2	Sequence 2, App1
39	204.5	11.4	1130	6	US-10-108-603-301	Sequence 301, App1
40	203	11.3	292	7	US-60-366-892-10	Sequence 10, App1
41	203	11.3	304	7	US-60-365-264-699	Sequence 699, App1
42	202	11.3	465	7	US-60-365-264-370	Sequence 370, App1
43	201	11.2	420	1	PCT-US02-13511-1	Sequence 1, App1
44	201	11.2	420	6	US-10-135-255-1	Sequence 1, App1
45	200.5	11.2	370	5	US-09-762-154-104	Sequence 104, App1

ALIGNMENTS

RESULT 1
US-09-573-655B-294
; Sequence 294, Application US/09573655B
; GENERAL INFORMATION:
; APPLICANT: SOLOVEY, Victor and TROUKHAN, Maxim
; TITLE OF INVENTION: Sequence-determined DNA Fragments and Corresponding Polypeptide
; FILE REFERENCE: 2750-0876P
; CURRENT APPLICATION NUMBER: US/09/573,655B
; NUMBER OF SEQ ID NOS: 3281
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 294
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-573-655B-294

Query Match
Best Local Similarity 14.78 Score 264; DB 5; Length 315;
Matches 89; Conservat 25.94 Pred. No. 5.4e-10;
Matches 89; Conservat 64; Mismatches 111; Indels 80; Gaps 16;

QY	11	ELIYNSAIDYTAIDKFNLPVCLK---IYDDEFSLPHSIREITFIKTLKPHNITE	67
DB	20	EKVEGCTGKYRAREKATGIVALKTRLHDEBEGVPTTLREISILMLARPHIYR	78
QY	68	YENDLK-----IYDVIIVTKLYRYDLSQLEITRYCKRTTFIYGINLVNQ	117
DB	79	LM-DVKQGINKEGTVY---LWFEVYDYLKKEFI-----RSRPR	113
QY	118	YTLNTEIERKIKMLMSGSEFIHSOGIIRHDKPSNIFPARDITOPITGPDICY	177
DB	114	-QAGCNIPQNTYVKCLMQLCKGMAFGCHGYLRDLKPHMLDRKTMFLKLA-----	165
QY	178	DLKLPKDEPMARYI-DVSTGYIKAPDLIGTINVEYEDISGLIITGLYSENFQSV	236
DB	166	DLGLARAFATLLPMKRYTHIELILWYRAPEVLIGATHTVGWDMVSCVIAELVTK--QAI	223
QY	237	LVKDQKELTNSHVSQDYLQINQIFENGFTGNLDFEDELPCDEYNMNHFFKFNQKYP	296
DB	224	FAGD-----SELDQLIRIRLLIGTP-----EVPQVSKLDWH-----EYP	261
QY	297	RKDW-----DILPRCNDLMLKEITFMIRYDSKRTSKITSEILO	335
DB	262	Q--WKPLSLSTAVPNL-DEAGDILSKMLEVEPAKRISAKKAME	302
RESULT	2		


```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-366-892-6
```

```
Query Match          13.4%; Score 240.5; DB 7; Length 297;
Best Local Similarity 25.4%; Pred. No. 1.5e-08;
Matches 85; Conservative 61; Mismatches 127; Indels 61; Gaps 14;
```

```
QY 7 YIDKELIYNSAIDITYAIDKFNPLPVCLK---IVDEDFSLPHSHREIFILTKLP 63
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   4 YRKIEIGGTVGVYKGRHKTGGVAMKRIELEEKGVSFAI-REISILKELR-HP 61

QY 64 NIIIEYNDKIYDD-VIIYTKLYRDLSQLIEIKYCKRTTFIYINGNLYNSQTYLAN 122
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   DB 62 NIVS-LQDVLMODSRLYLFEELSMCLKYLD-----STPPGQY----- 99

QY 123 EIEEKDIKMLKSMSSGLEFIHSGIIRHDIRPSNIFARDDITPIIGDPICYDLKLP 182
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   DB 100 -MDSLYKGYLVQILQGIYFCHSRRLHMDLKPQNLLI--DDKGTIKLADFLARAFGI- 155

QY 183 PKDEPPMAKYI-DVSTGIYKAPELLIGITNVEYIDWSLGIILGLSENQSVLVADD 241
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   DB 156 ----PIRYVTHEVTVLWRSPEVLGSAARYSPVDIWSIGTIFAEELAKR----- 200

QY 242 KETLN-DSHVSDLYLNOJFENNGTGNLDFEDELFCDEYNNENLHFKKFNLOKYPKDW 300
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   DB 201 KPLFHDSELDOLF---RIFRALGTNNNEWPEVESLDQYKNTFPKWKGLASHVKN-- 255

QY 301 DILLPRCNDLMKEIFTKMIRYDRSKRTSKEIL 334
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   DB 256 -----LDENGIDLKMLIYDPAKRISGMAL 282
```

```
RESULT 8
US-60-366-892-38
; Sequence 38, Application US/60366892
; GENERAL INFORMATION:
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: SUNESIS.006PR
; CURRENT APPLICATION NUMBER: US/60/366,892
; CURRENT FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-366-892-38
```

```
Query Match          13.2%; Score 236.5; DB 7; Length 427;
Best Local Similarity 24.5%; Pred. No. 3.9e-08;
Matches 91; Conservative 55; Mismatches 111; Indels 115; Gaps 17;
```

```
QY 14 YNSAISD-IYTAIDKFNPL-----VCLKIVDEDFSLPHS--I 49
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   DB 11 YSVEIGSTFTVLKRYQNLKPIGSAQIYCAAYDALIERNVAIKLSRPFQNGTHAKRA 70

QY 50 HREIFILTKLPNIIIEYN-----DLKIYDVILYTKLYRDLSQLIEIKYCKRTT 103
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   DB 71 YRELVLKRCVN-HKNIIGLVNFTPOKSLFEPDVIYVLMELMANLCQVIQW----- 121

QY 104 RFIYINGNLYNSQTYLANIEEKDIKMLKSMSSGLEFIHSGIIRHDIRPSNIFEAR 163
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   DB 122 -----ELDERMSYLYLQMLCGIKHHSAGIIRHDLKPSNI-VVKS 161

QY 164 DITPIIGDPICYDLKLPKDEPPMAKYIDVSTGIYKAPELLIGITNVEYIDWSLGI 223
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
DB 162 DCTLKIID-----FGLARFAGTSFMMTPY--VTRYRYRADEVILGM-GYKENVDIMSVCC 213

QY 224 ILTGLYSENFQSVLYKDKDELINDSHVSDLYLNOJFENNGTGNLDFEDELFCDEYNE 283
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   DB 214 IMGEMVCH-----KILPFGROYIDQW--NKVIEQLGTP-----CPFE---- 248

QY 284 NLHFKKF-----NLQKYPKRW-----DIIIP-----RCNDLMKEIFTKMIRYD 323
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   DB 249 ---MKLQPTVRYRYVENRPRYAGYSFEKLEPPDVLFPADSEHNKLKASQARDLSKMLVID 305

QY 324 RSKRTSKEILQ 335
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   DB 306 ASKRISYDEALQ 317
```

```
RESULT 9
US-60-366-892-43
; Sequence 43, Application US/60366892
; GENERAL INFORMATION:
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: SUNESIS.006PR
; CURRENT APPLICATION NUMBER: US/60/366,892
; CURRENT FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-366-892-43
```

```
Query Match          13.1%; Score 235; DB 7; Length 360;
Best Local Similarity 24.6%; Pred. No. 4e-08;
Matches 84; Conservative 66; Mismatches 127; Indels 64; Gaps 13;
```

```
QY 2 KLSVDYIDKELIYNSAIDITYAIDKFNPLPVCLKIVDEDFSLPHS--IHRREIFILTKL 59
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   DB 19 EYPERYQNLSPVSGAGVCAAFDTGTLGVAVKXLSRPOSIIHAKRTYRELRLKHM 78

QY 60 KHPNIIIEYN-----DLKIYDVILYTKLYRDLSQLIEIKYCKRTTFIYINGNL 113
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   DB 79 K-HENVIGLDLVETPARSLIEFNVDYLVTHMGADLNNIYK---COKLT----- 123

QY 114 VSNQTYLANIEEKDIKMLKSMSSGLEFIHSGIIRHDIRPSNIFARDDITPIIGDE 173
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   DB 124 -----DHRVQPLIYQILRGKLYHSADIIHRDLKPSNU-AVNEDCELKIL--- 167

QY 174 DICVDLKLPPKDEPPMAKYIDVSTGIYKAPELLIGITNVEYIDWSLGIILGLYSENF 233
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   DB 168 ---DFGLARHTDDEMTGY--VATRWYRAPPEIMLNMHNYNQTYDWSGCIW----- 213

QY 234 QSVLYKDKDELINDSHVSDLYLNOJFENNGTGNLDFEDELFCDEYNNENLHFKKFN 293
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   DB 214 -AELLTGTLPFGDHDIDQLKILRL--VGTPGA-----ELL-KKISSASARNYIOSLT 263

QY 294 KYPRKDWIILPRCNDLMKEIFTKMIRYDRSKRTSKEIL 334
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   DB 264 QMFKNMFANVFIGAN-PLAVDLLEKMLVLVDSDKRTTAQAL 303

RESULT 10
US-09-909-650A-24
; Sequence 24, Application US/09909650A
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Inc.
; APPLICANT: Maury, Isabelle
; APPLICANT: Zhou-Liu, Qing
; APPLICANT: Desanlis-Cremond, Francine
; TITLE OF INVENTION: New Polypeptides Derived From JNK3
; FILE REFERENCE: ST99003-US-CMT-1
```


Db 366 -VGRHSRKPWTKFINSQNLAVPEAVDFVDKLRYDHQERPTAKEM 412

RESULT 13
PCT-US02-13142-8265

; Sequence 8265, Application PC/TUS0213142

; GENERAL INFORMATION:

; APPLICANT: Elitira Pharmaceuticals, Inc.

; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and

; FILE REFERENCE: 10182-018-228

; CURRENT FILING DATE: 2002-04-23

; PRIOR FILING DATE: 2001-04-23

; PRIOR FILING DATE: 2001-04-23

; PRIOR FILING DATE: 2001-04-23

; PRIOR FILING DATE: 2001-04-23

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; PRIOR FILING DATE: 2001-04-23

; PRIOR FILING DATE: 2001-04-23

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; PRIOR FILING DATE: 2001-04-23

; PRIOR FILING DATE: 2001-04-23

; PRIOR FILING DATE: 2001-04-23

; FILE REFERENCE: 10182-018-999

; CURRENT APPLICATION NUMBER: US/10/128,714

; CURRENT FILING DATE: 2002-04-23

; PRIOR APPLICATION NUMBER: US 60/285,697

; PRIOR FILING DATE: 2001-04-23

; PRIOR APPLICATION NUMBER: US 60/287,066

; PRIOR FILING DATE: 2001-04-27

; PRIOR APPLICATION NUMBER: US 60/295,890

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/303,899

; PRIOR FILING DATE: 2001-07-09

; PRIOR APPLICATION NUMBER: US 60/316,362

; PRIOR FILING DATE: 2001-08-31

; NUMBER OF SEQ ID NOS: 8603

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8265

; LENGTH: 323

; TYPE: PRT

; ORGANISM: Aspergillus fumigatus

US-10-128-714-8265

Query Match 12.5%; Score 224.5; DB 6; Length 323;

Best Local Similarity 24.5%; Pred. No. 1.6e-07;

Matches 82; Conservative 67; Mismatches 123; Indels 63; Gaps 16;

Db 7 YIDKELIYNSAIDYTAIDKFNMLPVCLKIYDEDFSLPHSHIRIEIFLKLKHPNII 66

19 YKARELTHPNRI-----VALK-----IRLEAEDEGVSTAI-REISLKEMS-DPNIV 65

Db 67 EYFNDL-----KIYDVILVTIKLYRDLSQLIEITKCKRTTRFYIGINGNLVSNQYTLA 121

66 RLNIIVADGHKLY-----LVFEFLDLKLKYKALPVSE-----GGKSKALPESALS 114

Db 122 NEIEEKD--IKLWKSMSGLEFIHSQGIHRDIKPSNIFFARDITQPIIGDFDICYDL 179

115 KNNGLGDAMWKKFMAQLVEGIRYCHSHRILHRDLKPKQNLIDRDGMLK--LADFGIARAF 172

Db 180 KLPKDEPPMAKTI-DVSTGIYKAPRLIGITNYEYEDIDWSIGIILTGYSNFSQSVLY 238

173 GV-----PLRTYTHEVVTLMYRSPPELLLGROYSTGVDMSCGALFADMCYTR----- 219

Db 239 KDDKEL-TNDSHVSDDLNOIFENFGTPNLDFEDELFCDEYNNENLHKKFNLOKYPR 297

220 ---KPLPGDSEIDEIF---KIFGLGTDPDTTWPGVTSFPDY-----KTFPKMKR 265

Db 298 KDWIDILPRCNDLMEKIFTKMIRYDRSKRITSKE 332

266 QDPHTLVGLIEDGL-DLLEALLLEYDPARRISAKQ 299

RESULT 15

US-10-102-806-490

; Sequence 490, Application US/10102806

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, proteins and Antibodies

; FILE REFERENCE: PA103PIC1

; CURRENT APPLICATION NUMBER: US/10/102,806

; PRIOR FILING DATE: 2002-03-22

; PRIOR APPLICATION NUMBER: 09/925,298

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05881

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 846

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 490

; LENGTH: 527

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 29, 2002, 09:55:26 ; Search time 13.07 Seconds
(without alignments)
633.533 Million cell updates/sec

Title: US-09-072-994A-14

Perfect score: 1 MKLSYRDKELIINSAISD.....IRDRSKRIITSKILLQMLD 339

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgnt2_6/prodata/2/1aa/5A.COMB.pep:*
2: /cgnt2_6/prodata/2/1aa/5B.COMB.pep:*
3: /cgnt2_6/prodata/2/1aa/5A.COMB.pep:*
4: /cgnt2_6/prodata/2/1aa/5B.COMB.pep:*
5: /cgnt2_6/prodata/2/1aa/5A.COMB.pep:*
6: /cgnt2_6/prodata/2/1aa/5B.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	263.5	14.7	416	3	US-08-554-385-21 Sequence 21, Appl
2	262	14.6	391	4	US-09-131-028A-4 Sequence 4, Appl
3	262	14.6	391	4	US-09-131-028A-14 Sequence 14, Appl
4	261	14.6	298	2	US-08-874-347-25 Sequence 25, Appl
5	261	14.6	298	2	US-08-969-106-2 Sequence 2, Appl
6	261	14.6	298	2	US-09-093-522-25 Sequence 25, Appl
7	258.5	14.4	294	2	US-08-874-347-26 Sequence 26, Appl
8	258.5	14.4	294	2	US-09-093-522-26 Sequence 26, Appl
9	255.5	14.3	297	2	US-08-874-347-22 Sequence 22, Appl
10	255.5	14.3	297	2	US-09-093-522-22 Sequence 22, Appl
11	255.5	14.3	382	4	US-09-025-580-29 Sequence 29, Appl
12	255.5	14.3	424	3	US-09-209-668-17 Sequence 17, Appl
13	255.5	14.3	424	3	US-09-12913A-18 Sequence 18, Appl
14	254.5	14.2	424	5	PCT-US94-12913A-18 Sequence 32, Appl
15	254.5	14.1	365	4	US-09-025-580-32 Sequence 27, Appl
16	251.5	14.0	365	4	US-08-674-612-2 Sequence 2, Appl
17	251.5	14.0	365	4	US-08-920-296-2 Sequence 2, Appl
18	251.5	14.0	365	4	US-09-124-163-2 Sequence 2, Appl
19	248.5	13.9	384	4	US-09-025-580-35 Sequence 35, Appl
20	248.5	13.9	427	4	US-09-025-580-36 Sequence 36, Appl
21	247.5	13.8	382	4	US-09-025-580-30 Sequence 30, Appl
22	247.5	13.8	424	4	US-09-025-580-31 Sequence 31, Appl
23	246.5	13.8	365	2	US-08-746-788-2 Sequence 2, Appl
24	246.5	13.8	365	2	US-09-189-602-2 Sequence 26, Appl
25	246.5	13.8	365	4	US-09-025-580-26 Sequence 9, Appl
26	246	13.7	317	1	US-08-463-090B-9 Sequence 18, Appl
27	246	13.7	317	2	US-08-874-347-18 Sequence 18, Appl

28	246	13.7	317	3	US-09-093-522-18 Sequence 18, Appl
29	243.5	13.6	375	2	US-08-837-593-5 Sequence 5, Appl
30	243	13.6	360	3	US-08-554-385-20 Sequence 20, Appl
31	243	13.6	387	2	US-08-837-593-4 Sequence 4, Appl
32	241	13.5	371	2	US-08-837-593-6 Sequence 6, Appl
33	240.5	13.4	297	2	US-08-874-347-24 Sequence 24, Appl
34	240.5	13.4	297	3	US-09-093-522-24 Sequence 23, Appl
35	238.5	13.3	297	2	US-08-874-347-23 Sequence 23, Appl
36	238.5	13.3	297	1	US-09-093-522-23 Sequence 16, Appl
37	237.5	13.3	297	1	US-08-176-620A-16 Sequence 16, Appl
38	237.5	13.3	297	2	US-08-461-985-16 Sequence 7, Appl
39	237	13.2	370	4	US-08-837-593-7 Sequence 14, Appl
40	237	13.2	422	4	US-09-025-580-3 Sequence 14, Appl
41	236.5	13.2	353	1	US-08-176-620A-14 Sequence 14, Appl
42	236.5	13.2	353	2	US-08-461-985-14 Sequence 14, Appl
43	236.5	13.2	384	3	US-09-209-668-15 Sequence 15, Appl
44	236.5	13.2	384	4	US-09-025-580-33 Sequence 33, Appl
45	236.5	13.2	384	5	PCT-US94-08119-12 Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-554-385-21
; Sequence 21, Application US/08554385
; Patent No. 6017692
GENERAL INFORMATION:
APPLICANT: Roger Brent
APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,385
FILING DATE: No. 6017692member 8, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Karen F. Lech
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/252001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SDO ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-554-385-21
Query Match 14.7%; Score 263.5; DB 3; Length 416;
Best Local Similarity 23.7%; Pred. No 7, 7e-16;
Matches 86; Conservative 66; Mismatches 98; Indels 113; Gaps 14;

APPLICANT: Gustafson, Michael P.
TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
TITLE OF INVENTION: CARINII
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C., P.A.
STREET: 60 South Sixth Street, Suite 3300
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,347
FILING DATE: 13-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07039/055001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-335-5070
TELEFAX: 612-288-9696
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-874-347-25

Query Match 14.6%; Score 261; DB 2; Length 298;
Best Local Similarity 26.2%; Pred. No. 8.2e-16;
Matches 83; Conservative 59; Mismatches 119; Indels 56; Gaps 11;
QY 21 IYTAIDKFNPLPVCLKIV--DEDSLPHSHHREIFLTKLPHNPIEFNDKLYDOV 78
DB 18 YKRNKKTGGEVALKRIKIDTETEGVSTAIRISILKELN--HPNIVKLLDVIHTEKTL 76
QY 79 ILVTKLYRYSQLEITKYCKRTTRFYGINGNLVSNQYTLANEIEEKDKIKMLKSMSS 138
DB 77 YLVEFELHQDLKRFMDASA-----LTGIPPLP-----IKSYLFOQLQ 113
QY 139 GLEFHSOGIIRHDIKSNIFPARDITOPIDFQICVDKLPKDEPPMAKTI--DVST 197
DB 114 GLAFCHSHRVLRHDLKPNLINTGAIR--LADFGIARAFGV-----PVRTYTHEVYT 165
QY 198 GIYKAPELILGITYVEEIDIMSLGILTLGLYSENFQSVLVKDKDELTDNSHVSQLYLN 257
DB 166 LMYRAPPELLLSKYSTAVDIMSICIF-----AEAVYTRALFPDSEIDOLF--- 213
QY 258 QIFENEGTPNLTDEDELFCDEYNNENLHFKKFNLOKYPKXMDIILPCNDLMKEIFT 317
DB 214 RIFRTLGTPDEVVMPGVTSMPDY-----KPSFPMARQDSKVVPPLDED--GRSLLS 264
QY 318 KMIRYDRSKRITSKEIL 334
DB 265 QMLHYDPKRIKISAKAAL 281

RESULT 5
US-08-969-106-2
Sequence 2, Application US/08969106
Patent No. 5986055
GENERAL INFORMATION:
APPLICANT: Yang, M.

APPLICANT: Mandabalan, K.
TITLE OF INVENTION: CDK2 INTERACTIONS
TITLE OF INVENTION: CARINII
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennile & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,106
FILING DATE: 13-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-057
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-969-106-2

Query Match 14.6%; Score 261; DB 2; Length 298;
Best Local Similarity 26.2%; Pred. No. 8.2e-16;
Matches 83; Conservative 59; Mismatches 119; Indels 56; Gaps 11;
QY 21 IYTAIDKFNPLPVCLKIV--DEDSLPHSHHREIFLTKLPHNPIEFNDKLYDOV 78
DB 18 YKRNKKTGGEVALKRIKIDTETEGVSTAIRISILKELN--HPNIVKLLDVIHTEKTL 76
QY 79 ILVTKLYRYSQLEITKYCKRTTRFYGINGNLVSNQYTLANEIEEKDKIKMLKSMSS 138
DB 77 YLVEFELHQDLKRFMDASA-----LTGIPPLP-----IKSYLFOQLQ 113
QY 139 GLEFHSOGIIRHDIKSNIFPARDITOPIDFQICVDKLPKDEPPMAKTI--DVST 197
DB 114 GLAFCHSHRVLRHDLKPNLINTGAIR--LADFGIARAFGV-----PVRTYTHEVYT 165
QY 198 GIYKAPELILGITYVEEIDIMSLGILTLGLYSENFQSVLVKDKDELTDNSHVSQLYLN 257
DB 166 LMYRAPPELLLSKYSTAVDIMSICIF-----AEAVYTRALFPDSEIDOLF--- 213
QY 258 QIFENEGTPNLTDEDELFCDEYNNENLHFKKFNLOKYPKXMDIILPCNDLMKEIFT 317
DB 214 RIFRTLGTPDEVVMPGVTSMPDY-----KPSFPMARQDSKVVPPLDED--GRSLLS 264
QY 318 KMIRYDRSKRITSKEIL 334
DB 265 QMLHYDPKRIKISAKAAL 281

RESULT 6
US-09-093-522-25
Sequence 25, Application US/09093522
Patent No. 6015700
GENERAL INFORMATION:
APPLICANT: Limper, Andrew H.

APPLICANT: Leof, Edward B.
APPLICANT: Gustafson, Michael P.
TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
TITLE OF INVENTION: CARINITI
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C., P.A.
STREET: 60 South Sixth Street, Suite 3300
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093.522
FILING DATE: 08-JUN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/874,347
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07039/055002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-335-5070
TELEFAX: 612-288-9696
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-093-522-25

Query Match 14.6%; Score 261; DB 3; Length 298;
Best Local Similarity 26.2%; Pred. No. 8.2e-16;
Matches 83; Conservative 59; Mismatches 119; Indels 56; Gaps 11;
QY 21 IYVAKFNNLPVCLKIV--DEDESLPPHSIHREIFILTKLPHPNIIYFNDLKIYDV 78
DB 18 VYAKRKLGVEYVALKRIIDTEEGVSTAIRISLKELN-HPIVVLDDVHTENKL 76
QY 79 IIVTKLYRDLSQLIEITRYCKRTTREFIYGINGLVSNQYTLANEIEEKDIKLMKSMSS 138
DB 77 YIVFEELHDLKFKMDASA-----LIGIPLP-----IKSYLFOLQ 113
QY 139 GLEFIHSQGIHHDIKPSNIFFARADITQPIIGDPICVDKLPKDEPPMKYI-DVST 197
DB 114 GLAFCSHRYLRDLKPPNLLINTFESAIK--LADFGLARAFGv-----PVRTYTHEVVT 165
QY 198 GYKAPBELIGITNYEYEDIMSLGIIILGLYSENFOSVLYVDKDELINDSHVSDLYLNL 257
DB 166 LWRAPBILLSKYSTAVDWSLGLIF-----AEMVIRRALFPDSDSEIDOLF-- 213
QY 258 QIFENFGTPNLDFEDELFCDEYNNENLHFKKFNLOKYPKQMDIILPFCNDLKEIT 317
DB 214 RIFRTIGTPEVAVWPGVTSMPDY-----KSPFKMARODPSKVVPPLDED-GRSLLS 264
QY 318 KMIYRDSKRITSKEIL 334
DB 265 QMLHYDPNKRISAKAAL 281

RESULT 7

US-08-874-347-26
Sequence 26, Application US/08874347
Patent No. 5863741
GENERAL INFORMATION:
APPLICANT: Limper, Andrew H.
APPLICANT: Leof, Edward B.
APPLICANT: Gustafson, Michael P.
TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
TITLE OF INVENTION: CARINITI
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C., P.A.
STREET: 60 South Sixth Street, Suite 3300
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,347
FILING DATE: 13-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07039/055001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-335-5070
TELEFAX: 612-288-9696
TELEX:
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-874-347-26

Query Match 14.4%; Score 258.5; DB 2; Length 294;
Best Local Similarity 25.3%; Pred. No. 1.4e-15;
Matches 85; Conservative 60; Mismatches 132; Indels 59; Gaps 12;
QY 5 DYVIDKELIYSAISDIYTAIDKFNPLPVCLK--IVDEDESLPPHSIHREIFILTKLP 61
DB 2 EYKEKEKIGGTGYVYRADKYNLTETALKIRLQEDGVSSTAI-REISLKEMH- 59
QY 62 HPNIIYFNDLKIYDVILVTKLYRDLSQLIE-ITRYCKRTTREFIYGINGLVSNQYTL 120
DB 60 HGNIVRLHDVISHKRIYLVFEYLDLKKFMDSCPEFANPVL----- 103
QY 121 ANEIEEKIKIMLMSGSGLEFIHSQGIHHDIKPSNIFFARADITQPI-IGDPICVDL 179
DB 104 -----IKSYLVQLINGVAVCHSHRYLRDLKPPNLLT--DRTNALKLADFGLARAF 153
QY 180 KLPPDEPPMAKYIDVSGYKAPBELIGITNYEYEDIMSLGIIILGLYSENFOSVLYK 239
DB 134 GIVAVTFTH-----EYVILWRAPBILLSKYSTAVDWSLGLIF-----AEMVN 199
QY 240 DDELJNDSHVSDLYLNLQIFENFGTPNLDFEDELFCDEYNNENLHFKKFNLOKYPKQ 239
DB 200 QKPLFPDSEIDOLF--KIRRVILGTPMEQSWPVGSSLPDY-----KSAPFKWQAO 248
QY 300 WDIILPFCNDLKEITKMIYRDSKRITSKEILO 335
DB 249 IATIVPTL-DPAGLDLSKMLRYEPNKRITARAOLE 283

DB 209 LPPGSEIDEIF---KIFOVLTGTPNEEVPVTLLODYKSTFPPRKRMDLHK----- 257

QY 303 ILPRCNDLMKEIFTKMIRYDRSKRITSKEILO 335

DB 258 VVNGEEDAI-ELLISAMLYDPAHRISAKRALQ 289

RESULT 10

US-09-093-522-22

; Sequence 22, Application US/09093522

; Patent No. 6015700

; GENERAL INFORMATION:

; APPLICANT: Limper, Andrew H.

; APPLICANT: Leof, Edward B.

; APPLICANT: Thomas, Charles F.

; APPLICANT: Gustafson, Michael P.

; TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C., P.A.

; STREET: 60 South Sixth Street, Suite 3300

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/093.522

FILING DATE: 08-JUN-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/874.347

FILING DATE: 13-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ellinger, Mark S.

REGISTRATION NUMBER: 34.812

REFERENCE/DOCKET NUMBER: 07039/055002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-335-5070

TELEFAX: 612-288-9696

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 297 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-093-522-22

Query Match 14.3%; Score 255.5; DB 3; Length 297;

Best Local Similarity 24.3%; Pred. No. 2.6e-15;

Matches 81; Conservative 70; Mismatches 131; Indels 51; Gaps 11;

QY 7 YIDKEIIVSAISDIYTAIDKFNMLPVCLK---IYDEDESLPHSHIREIFILKTLKPH 63

DB 4 YQKVERIGEGYGVVYKARHKLGRIVAMKIRLEDESEGVSTAI-REISLKEVNDEN 62

QY 64 NIEFYNDKIYDVILVTKRYDLSQLEIFTKYCKRTTFTYINGNMLVSNQYTLANE 123

DB 63 N---RNCRCRLDILHAESKIVYFEFLDMDLKYMDRISF-----TGATS 105

QY 124 IEKDKILMLKSMSSGLEFIHSGIIRHDIKPSNIFPANDITQPIIGFDICYDKLP 183

DB 106 LDRILVQKFTYQLVNGVNCFSRRIIHRDLKPONLLIDREGNLK--LADFGIARSGV-- 161

QY 184 KDEPPAKYI-DVSTGIYKAPELLIGITVNEYEIDIMSIGIILTGLYSENFOSVLVKDK 242

DB 162 ----PLRNYHEIYTLVYARPEVLGSRHYSQVDIWSVGLF-----AKMIRSP 208

QY 243 ELTNDHSVSDLYLLNOIFENFGTPNLTDEDELFCDEYNENENLHKKNLQKYPKKWDI 302

DB 209 LPPGSEIDEIF---KIFOVLTGTPNEEVPVTLLODYKSTFPPRKRMDLHK----- 257

QY 303 ILPRCNDLMKEIFTKMIRYDRSKRITSKEILO 335

DB 258 VVNGEEDAI-ELLISAMLYDPAHRISAKRALQ 289

RESULT 11

US-09-025-580-29

; Sequence 29, Application US/09025580

; Patent No. 6162613

; GENERAL INFORMATION:

; APPLICANT: Su, Michael Shin-San

; APPLICANT: Fox, Ted

; APPLICANT: Wilson, Keith Phillip

; APPLICANT: Hermann, Ursula A.

; TITLE OF INVENTION: Methods For Designing Inhibitors of

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: US

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025.580

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Haley, James F.

REGISTRATION NUMBER: 27.794

REFERENCE/DOCKET NUMBER: VPI 97-104

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9090

TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 382 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-025-580-29

Query Match 14.3%; Score 255.5; DB 4; Length 382;

Best Local Similarity 27.1%; Pred. No. 3.6e-15;

Matches 92; Conservative 49; Mismatches 112; Indels 87; Gaps 16;

QY 21 IYTAIDKFNMLPVCLKIVDEDESLPHS--IHREIFILKTLKPHNPITIEFN-----DL 72

DB 40 VCAAFDVLVIGISAVVAKLSRPFQNHAKRAVRELVILKCVN-HKNIISLVNFTQKIL 98

QY 73 KIYDVLIVTKRYDLSQLEIFTKYCKRTTFTYINGNMLVSNQYTLANEIEKDKIM 132

DB 99 EEPQDYIVYMLMDANLCQYIHM-----ELDHRSYTL 131

QY 133 LKSMSSGLEFIHSGIIRHDIKPSNIFPANDITQPIIGFDI---CYDLKLPKDEPP 188

DB 132 LYQMLCGIKHLSAGIIRHDIKPSNI-VVKSDCITLIL-DGILARACTGFMMPY---- 185

```

RESULT 13
PCT-US94-12913A-18
: Sequence 18: Application PC/TUS9412913A
: GENERAL INFORMATION:
: APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
: APPLICANT: UNIVERSITY OF MASSACHUSETTS MEDICAL SCHOOL
: APPLICANT: Katin, Michael
: APPLICANT: Davis, Roger
: APPLICANT: Hibi, Masahiko

```

RESULT 14
US-09-025-580-32
; Sequence 32, Application US/09025580
; Patent No. 6162613
; GENERAL INFORMATION;

APPLICANT: Su, Michael Shin-San
APPLICANT: Fox, Ted
APPLICANT: Wilson, Keith Phillip
APPLICANT: German, Ursula A.
TITLE OF INVENTION: Methods For Designing Inhibitors of
SERINE/THREONINE KINASES AND TYROSINE KINASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,580
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: VPI 97-104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-580-32

Query Match 14.2%; Score 254.5; DB 4; Length 424;
Best Local Similarity 27.1%; Pred. No. 5.1e-15;
Matches 92; Conservative 49; Mismatches 112; Indels 87; Gaps 16;
21 IYAIIDFNNLPVCLKIVDEDFSLPHPS--IHREIFILTKLPHNIIIEFN-----DL 72
40 VCAAFDVLGINAVKLSRPQNOHAKRAYRELVLKCVN-HKNIISLVNFTFOKTL 98
73 KIYDVLVTKLYRDLISQLEITKYCKRTTRFIYINGNLVSNQYTLANEIPEKDIKLM 132
99 EEFODVYLVLMELDANLCQVIM-----ELDHKMSYL 131
133 LKMSGSLERFHSOGIIRHRIKPSNIFFARDITOPITIGDFI-----CYDLKLPDDEPP 188
132 LYOMCGIKLHSGAGIIRDLKPSNI-VKSDCTLKIL-DFGLARACTINFMATPY----- 185
189 MAKYIDVSTGIYKAPELLIGITNYEYEDIMSLGIIITGLYSNFOSVLWKDKELTND 248
186 -----VYTRRYRAPEVILDM-GYKENVDIMSYGCI-----GELVKGCVIFQGD 229
249 HVSDDLVLNIOIFENFGPNLTDFEDELFCDEYNNENLHFKKFLQKPYR-----KDM 301
230 HIDD---WNKYIEQLGTPS-AEFKKKLOPTVRNVE-----NRPKYGIKFEELPDM 278
302 IILP-----RCNDLMEKEIFTKMIRYDRSKRITSKEILQ 335
279 -IFPSESEDRKITSQARDLSKMLVLDPPKRISVDEALR 317

RESULT 15
US-09-025-580-27
Sequence 27, Application US/09025580
Patent No. 6162613

GENERAL INFORMATION:
APPLICANT: Su, Michael Shin-San
APPLICANT: Fox, Ted
APPLICANT: Wilson, Keith Phillip
APPLICANT: German, Ursula A.
TITLE OF INVENTION: Methods For Designing Inhibitors of
SERINE/THREONINE KINASES AND TYROSINE KINASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,580
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: VPI 97-104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-580-27

Query Match 14.1%; Score 252.5; DB 4; Length 365;
Best Local Similarity 26.1%; Pred. No. 6.3e-15;
Matches 90; Conservative 57; Mismatches 125; Indels 73; Gaps 14;
2 KLSIDYIDKELIYNSAISDIYTAIDKRNPLVCLKIYDEDF--SLPHSHIREIFILTKL 59
20 ELPKTYVSPTHVSGAGVSCSAIDKRGSEKVAITKLSRPQSEIFAKRAYRELLKHM 79
60 KPHNII--EYF--NDKIYDVLVTKLYRDLISQLEITKYCKRTTRFIYINGNL 113
80 Q-HENVIGLIDVFPASSLRNFYDILVMPMDLQKI----- 117
114 VSNQYTLANEIEKDIKLMKSMSSGLEFIHSGIIRHRIKPSNIFFARDITOPITIGDF 173
118 -----MGMESEEEKIQVLVYQMLKGLYIHSAGVHRDLKPGML-AVNEDCEKIL- 167
174 DICVYLKLPKDEPMKAYIDVSTGIYKAPELLIGITNYEYEDIMSLGIIITGLY 229
168 -----DFGLARHADAMETGY--VYTRRYRAPEVILSMWHYNOTVIMSYGCIAMALTG- 219
230 SENFOSVLWKDKELTNDSHVSDYLLNIOIFENFGPNLTDFEDELFCDEYNNENLHFKK 289
220 -----KYLEKGDYIDQ-----LVQILKYGVCPG-TFEVQKL-----NDAKAS 259
290 FNLOKYPKRDMDIILPNCNDLMEKEIFTKMIRYDRSKRITSKEIL 334
260 QSLPQTPRKDFTQLPFPRAAPQ-AAULLKMLVDVDRKLTFAQAL 303

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